

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 30, 2004, 02:03:16 ; Search time 8287 Seconds
(without alignments)
12334.771 Million cell updates/sec

Title: US-10-092-390-1
Perfect score: 3423
Sequence: 1 atggttattttctttgaactc.....gcagcagcagcagtgaatga 3423

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	1334.2	39.0	3162	11	BC029999	BC029999	Homo sapi
2	992.6	29.0	2910	29	AY406554	AY406554	Homo sapi
3	972.6	28.4	3568	11	AK051642	AK051642	Mus muscu
4	933.2	27.3	2910	29	AY406556	AY406556	Mus muscu
5	892.6	26.1	3466	11	AK032661	AK032661	Mus muscu
6	653.6	19.1	2910	29	AY406555	AY406555	Pan trogl
7	646.2	18.9	3556	11	AK053551	AK053551	Mus muscu
8	587.6	17.2	789	14	CD803668	CD803668	UI-M-GV0-
9	539	15.7	921	13	BU215784	BU215784	603106167
10	530.4	15.5	755	14	CD802967	CD802967	UI-M-GV0-
11	508.6	14.9	643	13	BU056532	BU056532	UI-M-FO0-
12	470	13.7	2944	11	AK048840	AK048840	Mus muscu
13	456.6	13.3	755	12	BG828819	BG828819	602751395
14	433	12.6	565	12	BM719978	BM719978	UI-E-EJ0-
c 15	432	12.6	598	12	BM676825	BM676825	UI-E-EJ0-
16	417.4	12.2	846	13	BX741190	BX741190	
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18	398.8	11.7	798	13	BU112175	BU112175	603126134
19	379	11.1	538	10	BB762574	BB762574	BB762574
20	370	10.8	715	9	AI958909	AI958909	fd05g03.y
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22	366.8	10.7	779	10	BF529240	BF529240	602041695
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26	352.8	10.3	734	14	CF745181	CF745181	UI-M-GV0-
27	328.6	9.6	772	14	CF538219	CF538219	UI-M-GH0-
28	328.2	9.6	584	10	BF686873	BF686873	602102830
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31	309.4	9.0	1123	12	BM563529	BM563529	AGENCOURT
32	302	8.8	559	10	AW658138	AW658138	93921 MAR
33	301.2	8.8	563	14	CF538582	CF538582	UI-M-GI0-
34	296.2	8.7	937	10	BF180097	BF180097	601806458
35	294.4	8.6	852	9	AL040177	AL040177	DKFZp434F
36	293.2	8.6	401	10	BE664785	BE664785	152639 MA
37	283.4	8.3	451	14	CB786815	CB786815	AMGNNUC:N
38	282.2	8.2	463	10	AW445546	AW445546	81787 MAR
39	271.2	7.9	477	10	BF442243	BF442243	258883 MA
40	268.8	7.9	693	14	CF739003	CF739003	UI-M-HD0-
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42	255	7.4	634	13	BY726500	BY726500	BY726500
43	253.6	7.4	634	10	BB650216	BB650216	BB650216
44	251	7.3	843	13	BU282192	BU282192	603862751
45	250.2	7.3	600	14	CA893118	CA893118	B0177A01-

ALIGNMENTS

RESULT 1

BC029999

LOCUS BC029999 3162 bp mRNA linear HTC 06-MAY-2002

DEFINITION Homo sapiens, clone IMAGE:4156083, mRNA.

ACCESSION BC029999

VERSION BC029999.1 GI:20455873

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3162)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (06-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USAREMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: David N. Louis, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>Contact: amg@bcm.tmc.eduGunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 52 Row: a Column: 10

This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 14192940

This clone has the following problem: no 5' EST match.

FEATURES

source

Location/Qualifiers

1. .3162

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4156083"

/tissue_type="Brain, anaplastic oligodendroglioma with
1p/19q loss"

/clone_lib="NCI_CGAP_Brn67"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 39.0%; Score 1334.2; DB 11; Length 3162;
Best Local Similarity 69.4%; Pred. No. 0;
Matches 1845; Conservative 0; Mismatches 808; Indels 6; Gaps 2;

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Qy      74 CTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTACTCAGTGACTGTGC 133
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      229 CCCTGAACCCCGAGGACCCCAACGTGTGCAGCCACTGGGAGAGCTATGCTGTGACTGTCC 288

Qy      134 AAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGCACTGACATTCTAA 193
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      289 AGGAATCGTATGCACACCCCTTCGATCAGATCTATTACACACGATGCACAGACATCCTCA 348

Qy      194 ACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCTATCGACATGGGGAGA 253
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Db      349 ACTGGTTCAAGTGCACCAGGCACCGGATCAGTTATAAGACGGCGTATCGGAGAGGCCTCC 408

Qy      254 AGACTATGTATAGGCGCAAGTCTCAGTGTGTCTGGATTTTATGAAAGCGGGGAAATGT 313
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Db      409 GGACCATGTACCGGCGGAGGTCCCAGTGTGCTGCCCTGGCTACTATGAGAGCGGAGACTTCT 468

Qy      314 GTGTCCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTGCTCCAAACACCTGTC 373
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      469 GCATACCCCTGTGTACGGAGGAGTGTGTGCACGGCCGCTGCGTTTCCCCGGACACCTGCC 528

Qy      374 AGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGATGGTGATCACTGGG 433
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      529 ACTGCGAGCCTGGCTGGGGAGGGCCCCGACTGCTCCAGCGGCTGCGACAGCGACCACTGGG 588

Qy      434 GTCCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGCAACCCCATCACCG 493
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Db      589 GGCCCCCACTGCAGCAACCGGTGCCAGTGCCAGAACGGCGCCCTGTGTAACCCCATCACAG 648

Qy      494 GGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGACCGCTGTGAGCAGG 553
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Db      649 GCGCCTGCGTGTGCGCCGCCGGCTTCCGTGGATGGCGCTGCGAGGAGCTCTGCGCGCCTG 708

Qy      554 GCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATGGAGCCACCTGCGACC 613
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Db      709 GCACCCACGGCAAGGGATGCCAGCTGCCGTGCCAGTGCCGACACGGTGCCAGCTGCGACC 768

Qy      614 ACGTCACGGGGGAATGCCGCTGCCACCAGGATACACGGAGCCTTCTGTGAGGATCTTT 673
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      769 CCCGCGCCGGCGAGTGCCTCTGCGCACCTGGCTACACGGCGTCTACTGCGAGGAGCTGT 828

Qy      674 GTCCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGTCAAAATGGAGGAG 733
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      829 GCCCTCCTGGGAGCCATGGAGCTCACTGTGAGCTGCGCTGCCCCGTGTCAGAATGGGGGCA 888

Qy      734 TGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGATGGGCACAGTGTGTG 793
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Db      889 CCTGCCACCACATCACTGGCGAGTGTGCCTGCCCCCAGGCTGGACGGGAGCAGTGTGTG 948

Qy      794 GTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAATGCCAGTGCCATA 853
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Db      949 CCCAGCCCTGCCACCAGGGACATTTGGCCAGAAGTGCAGCCAGGATTGTCCTTGCCACC 1008

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Db	1009	ATGGAGGGCAGTGTGACCACGTGACTGGACAGTGCCACTGTACAGCTGGATACATGGGGG	1068
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Db	1069	ACAGGTGCCAAGAGGAGTGCCCTTCGGGTCCTTCGGCTTCCAGTGCTCACAGCGCTGTG	1128
Qy	974	AGTGTGTCAACGGAGGGAAGTGTTACCACGTGAGCGGCGCATGCCTCTGTGAAGCAGGCT	1033
Db	1129	ACTGCCACAATGGGGGGCAGTGTTACCCACCACGGGTGCCTGCGAGTGTGAGCCTGGCT	1188
Qy	1034	TTGCTGGCGAGCGCTGCCAAGCACGCCTGTGTCTTGAGGGGCTCTACGGCATCAAATGTG	1093
Db	1189	ACAAGGGCCACGCTGCCAGGAGCGACTGTGCCCGGAGGGCCTGCATGGCCCAGGCTGCA	1248
Qy	1094	ACAAACGGTGTCCCTGCCACTTGGAAAACACTCATAGCTGTACCCCATGTCTGGAGAGT	1153
Db	1249	CCCTGCCCTGCCCTGTGACGCTGACAACACCATCAGCTGCCACCCAGTAAGTGGAGCTT	1308
Qy	1154	GTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGTTCTCCTGGATTCT	1213
Db	1309	GTACCTGCCAGCCAGGCTGGTCTGGTCACCACTGCAATGAATCCTGCCCTGTTGGCTACT	1368
Qy	1214	ACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTGTGA	1273
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Qy	1274	CTGGAAAGTGACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACCCCATGCCCTC	1333
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Qy	1334	TGGGAACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAATGATGCAGTCTGCT	1393
Db	1489	CAGGGACCTATGGCCCCAACTGCTCGTCCATCTGTAGCTGTAACAATGGTGGCACCTGCT	1548
Qy	1394	CTCCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCACGGGGTGGACTGCTCCATCA	1453
Db	1549	CCCCAGTAGATGGCTCCTGTACCTGCAAGGAAGGGTGGCAGGGCCTGGACTGCACCCTGC	1608
Qy	1454	GATGTCCCAGTGGGCACATGGGGCTTTGGCTGTAACCTAACATGCCAGTGCCTCAACGGGG	1513
Db	1609	CATGTCCCAGTGGGACGTGGGGCCTGAACTGCAACGAGAGCTGCACCTGTGCCAATGGGG	1668
Qy	1514	GAGCCTGCAACACCTTGACGGGACCTGCACGTGTGCACCTGGATGGCGCGGGGAGAAAT	1573
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Qy	1574	GCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAGCGCTGCGACTGCA	1633
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Qy	1634	GCCACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTCCCGGGATGGTCAG	1693
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Db	1849	GCATCCGCTGTGACAGCACGTGTCCACCTTGGCCGCTGGGGCCCCAACTGCTCTGTCTCCT	1908
Qy	1754	GCTACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGCCAGTGTGCCACCAG	1813
Db	1909	GCAGCTGTGAGAATGGAGGCTCCTGCTCCCCAGAGGATGGGAGCTGCCAGTGTGCCCTTG	1968
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Db	1969	GCTTCCGAGGACCTTATGCCAGAGAATCTGCCCCCTGGGTTCCTATGGCCACGGCTGCG	2028
Qy	1874	GCCAGACATGCCCACAGTGC GTTCACAGCAGCGGGCCCTGCCACCACATCACCGGCCTGT	1933
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Qy	1934	GTGACTGCTTGCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGTCCAGTGGCAGAT	1993
Db	2089	GTGAGTGCCTCCAGGATTCTCTGGAGCTCTCTGCAACCAAGTGTGTGCTGGAGGATACT	2148
Qy	1994	TTGGGAAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACCTGTAACCCCATTG	2053
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Qy	2054	ACAGATCTTGTCACTGTTACCCCGGTTGGATTGGCAGTGA CTGCTCTCAACCATGTCCAC	2113
Db	2209	ATGGCTCCTGCCAGTGCCTTCTGGATGGATTGGCAAGGACTGCTCACAGGCTTGCCAC	2268
Qy	2114	CTGCCCCTGCGGGGCCAACTGCATCCACACGTGCAACTGCCATAATGGAGCTTTCTGCA	2173
Db	2269	CCGGGTTCTGGGGCCCCGCCTGCTTCCACGCATGCAGCTGCCACAACGGGGCGAGCTGCA	2328
Qy	2174	GCGCCTACGATGGGGAATGTAATGCACTCCTGGCTGGACAGGGCTCTACTGCACTCAGA	2233
Db	2329	GCGCCGAGGACGGGGCTGCCACTGCACCCCTGGCTGGACTGGACTCTTCTGCACACAGC	2388
Qy	2234	GATGTCCTCTAGGGTTTTATGGAAGATTGTGCACTGATATGCCAATGTCAAAACGGAG	2293
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Db	2449	CCAGCTGTGACCACATCAGTGGCAAGTGCACCTGCCGCAAGGCTTCACCGGGCAACACT	2508
Qy	2354	GTGAGCAGAAGTGCCCTTCAGGAACATATGGCTATGGCTGTGCGCCAGATATGTGATTGTC	2413
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Qy	2414	TGAACAACTCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGCCCCGGATGGAAGG	2473
Db	2569	TGAACAACTCCACCTGTGACCATGTCAACGGCACCTGTTACTGCAGCCCTGGCTTCAAAG	2628
Qy	2474	GAGCGAGATGTGATCAAGCTGGTGTATCATAGTTGGAAATCTGAACAGCTTAAGCCGAA	2533
Db	2629	GAATCAGGTGTGACCAAGCTGCCCTCATGATGGAGG---AGCTGAATCCCTACACCAAGA	2685
Qy	2534	CCAGTACTGCTCTCCCTGCTGATTCTTACCAGATCGGGGGCCATTGCAGGCATCATCATTC	2593
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Qy 2594 TTGTCCTAGTTGTTCTCTTCTACTGGCATTGTTTCATTATTATAGACACAAGCAGAAGG 2653
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 Db 2746 TGTTATTCCTCATTGTGGTGCTGCTGGGCCTATTTGCCTGGCATCGGCGGCGGCAGAAAG 2805
 Qy 2654 GAAAGGAATCAAGCATG---CCAGCAGTTACCTACACCCCTGCTATGAGGGTCGTCAATG 2710
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 Qy 2711 CAGATTATACCATTTCAGG 2729
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 Db 2866 CCGACTACTCCCTCTCAGG 2884

RESULT 2

AY406554

LOCUS AY406554 2910 bp DNA linear GSS 12-DEC-2003

DEFINITION Homo sapiens HCM2596 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY406554

VERSION AY406554.1 GI:39762525

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2910)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2910)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1..2910
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 gene <1..>2910
 /locus_tag="HCM2596"

ORIGIN

Query Match 29.0%; Score 992.6; DB 29; Length 2910;
 Best Local Similarity 57.8%; Pred. No. 2.3e-272;
 Matches 1396; Conservative 0; Mismatches 1013; Indels 6; Gaps 2;

Qy	318	CCCCCACTGTGCTGATAAATGTGTCCATGGTTCGCTGTATTGCTCCAAACACCTGTCAGTG	377
Db	75	CGCCCTGTGTACGGAGGAGTGTGTGCACGGCCGCTGCGTTTCCCCGGACACCTGCCACTG	134
Qy	378	TGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGATGGTGATCACTGGGGTCC	437
Db	135	CGAGCCTGGCTGGGGAGGGCCCGACTGCTCCAGCGNNNNNNNNNNNNNNNNNNNNNNNNNN	194
Qy	438	CCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGCAACCCCATCACCGGGC	497
Db	195	NN	254
Qy	498	TTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGACCGCTGTGAGCAGGGCAC	557
Db	255	NN	314
Qy	558	CTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATGGAGCCACCTGCGACCACGT	617
Db	315	NN	374
Qy	618	CACGGGGGAATGCCGCTGCCACCAGGATACACCGGAGCCTTCTGTGAGGATCTTTGTCC	677
Db	375	NN	434
Qy	678	TCCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGTCAAAATGGAGGAGTGTG	737
Db	435	TCCTGGGAGCCATGGAGCTCACTGTGAGCTGCGCTGCCCTGTGAGAATGGGGGCACCTG	494
Qy	738	TCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGATGGGCACAGTGTGTGGTCA	797
Db	495	CCACCACATCACTGGCGAGTGTGCCTGCCCCCAGGCTGGACGNNNNNNNNNNNNNNNNNN	554
Qy	798	GCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAATGCCAGTGCCATAATGG	857
Db	555	NN	614
Qy	858	AGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCAGGATACACAGGGGAACG	917
Db	615	NN	674
Qy	918	GTGCCAGGATGAGTGTCTGTGGGACCTATGGCGTTCTCTGTGCTGAGACCTGCCAGTG	977
Db	675	GTGCCAAGAGGAGTGCCCTTCGGGTCTTCGGCTTCCAGTGCTCACAGCGCTGTGACTG	734
Qy	978	TGTCAACGGAGGGAAGTGTACCACGTGAGCGGCGCATGCCTCTGTGAAGCAGGCTTTGC	1037
Db	735	CCACAATGGGGGGCAGTGTTCACCCACCACGGGTGCCTGCGAGTGTGAGCCTGGCTACAA	794
Qy	1038	TGGCGAGCGCTGCGAAGCACGCCTGTGTCCTGAGGGGCTCTACGGCATCAAATGTGACAA	1097
Db	795	GGGCCACGCTGCCAGGAGCGACTGTGCCCGAGGGCCTGCATGGCCCAGGCTGCACCCT	854
Qy	1098	ACGGTGTCCCTGCCACTTGAAAACACTCATAGCTGTACCCCATGTCTGGAGAGTGTGC	1157
Db	855	GCCCTGCCCCGTGTGACGCTGACAACACCATCAGCTGCCACCCAGTAAGTGGAGCTGTAC	914

Qy	1158	CTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGTTCTCCTGGATTCTACGG	1217
Db	915	CTGCCAGCCAGGCTGGTCTGGTCACCACTGCAATGAATCCTGCCCTGTTGGCTACTATGG	974
Qy	1218	GGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTGTGACTGG	1277
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Qy	1278	AAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACCCCATGCCCTCTGGG	1337
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Qy	1338	AACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAATGATGCAGTCTGCTCTCC	1397
Db	1095	GACCTATGGCCCCAACTGCTCGTCCATCTGTAGCTGTAACAATGGTGGCACCTGCTCCCC	1154
Qy	1398	TGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCACGGGGTGGACTGCTCCATCAGATG	1457
Db	1155	AGTAGATGGCTCCTGTACCTGCAAGGAAGGGTGGCAGGGCCTGGACTGCACCCTGCCATG	1214
Qy	1458	TCCCAGTGGGCACATGGGGCTTTGGCTGTAACCTTAACATGCCAGTGCCTCAACGGGGGAGC	1517
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Qy	1518	CTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGGCGCGGGGAGAAATGCGA	1577
Db	1275	CTGCAGCCCCATAGACGGCTCCTGCTCCTGCACTCCTGGCTGGCTGGGAGACACCTGTGA	1334
Qy	1578	ACTTCCCTGCCAGGATGGCACGTACGGGTGAACTGTGCTGAGCGCTGCGACTGCAGCCA	1637
Db	1335	GCTGCCTTGCCCGGATGGCACATTTGGGTGAACTGCAGTGAACACTGTGACTGCAGCCA	1394
Qy	1638	CGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTCCCGGGATGGTCAGGTGT	1697
Db	1395	TGCTGATGGATGTGACCCCGTCACAGGCCACTGCTGCTGCCTGGCCGGATGGACAGGCAT	1454
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Db	1455	CCGCTGTGACAGCACGTGTCCACCTGGCCGCTGGGGCCCCAACTGCTCTGTCTCCTGCAG	1514
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Db	1515	CTGTGAGAATGGAGGCTCCTGCTCCCCAGAGGATGGGAGCTGCGAGTGTGCCCTGGCTT	1574
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Db	1635	GCCATGCCCCCTCTGCGTGCACAGCAGAGCCCTGCCACCACATCAGCGGCATCTGTGA	1694
Qy	1938	CTGCTTGCCTGGCTTACAGGCGCCCTCTGCAATGAAGTGTGTCCAGTGGCAGATTTGG	1997
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Db	1755	GCAGGACTGTGCCAGCTCTGCTCCTGTGCCAACACGGGACCTGCAGCCCTATCGATGG	1814
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Db	1995	CCCAGCAGCATTTTTTGGGAAGGACTGTGGGCGCGTATGCCAGTGTGAGAATGGCGCCAG	2054
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Qy	2478	GAGATGTGATCAAGCTGGTGTATCATAGTTGGAAATCTGAACAGCTTAAGCCGAACCAG	2537
Db	2235	CAGGTGTGACCAAGCTGCCCTCATGATGGAGG---AGCTGAATCCCTACACCAAGATCAG	2291
Qy	2538	TACTGCTCTCCCTGCTGATTCTTACCAGATCGGGGCCATTGCAGGCATCATCATTTCTTGT	2597
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Qy	2598	CCTAGTTGTTCTCTTCCCTACTGGCATTGTTCAATTATTTATAGACACAAGCAGAAGGGAAA	2657
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Qy	2658	GGAATCAAGCATG---CCAGCAGTTACCTACACCCCTGCTATGAGGGTCGTCAATGCAGA	2714
Db	2412	GGGCCGAGACCTGGCTCCCCGTGTCTCTACACACCTGCCATGAGGATGACCAGCACCGA	2471
Qy	2715	TTATACCATTTCAGG	2729
Db	2472	CTACTCCCTCTCAGG	2486

RESULT 3

AK051642

LOCUS AK051642 3568 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130061K05 product:MEGF11 PROTEIN

(KIAA1781) homolog [Homo sapiens], full insert sequence.

ACCESSION AK051642

VERSION AK051642.1 GI:26342079

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3568)

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,

Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .3568
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:D130061K05"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="12 days embryo"

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/note="unnamed protein product; MEGF11 PROTEIN (KIAA1781)
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/db_xref="GI:26342080"
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ORIGIN

Query Match 28.4%; Score 972.6; DB 11; Length 3568;
Best Local Similarity 65.4%; Pred. No. 1.4e-266;
Matches 1495; Conservative 0; Mismatches 699; Indels 93; Gaps 1;

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RESULT 4

AY406556

LOCUS AY406556 2910 bp DNA linear GSS 12-DEC-2003

DEFINITION Mus musculus HCM2596 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY406556

VERSION AY406556.1 GI:39762527

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

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 Db 555 NNN 614

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 Db 615 NNN 674

Qy 918 GTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGTGCTGAGACCTGCCAGTG 977
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 Db 795 GGGCCCTAGCTGCCAGGAGCGGCTATGCCCTGAGGGCCTGCATGGCCAGGCTGCACCTT 854

Qy 1098 ACGGTGTCCCTGCCACTTGGAACACTCATAGCTGTCACCCCATGTCTGGAGAGTGTGC 1157
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 Db 855 GCCCTGCCCCGTGTGACACCGAGAACACTATCAGCTGCCATCCAGTTACTGGAGCTTGTAC 914

Qy 1158 CTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGTTCTCCTGGATTCTACGG 1217
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 Db 915 CTGCCAACCAGGCTGGTCTGGCCACTACTGCAATGAGTCCTGCCCCGCCGGCTACTATGG 974

Qy 1218 GGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTGTGACTGG 1277
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 Db 975 CAACGGTTGCCAGCTACCCTGCACCTGCCAGAACGGTGTGACTGCCACAGTATCACCGG 1034

Qy 1278 AAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACCCCATGCCCTCTGGG 1337
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 Db 1035 GAGCTGCACTTGTGCTCCAGGCTTCATGGGAGAGGTGTGTGCCGTCCCCTGTGCTGCAGG 1094

Qy 1338 AACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAATGATGCAGTCTGCTCTCC 1397
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 Db 1095 GACCTATGGTCCCAACTGTTTCTCTGTATGTAGCTGTAGCAACGGCGGCACCTGTTCCCC 1154

Qy 1398 TGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCAGGGGTGGACTGCTCCATCAGATG 1457
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Qy 1458 TCCCAGTGGCACATGGGGCTTTGGCTGTAACCTAACATGCCAGTGCCCTAACGGGGGAGC 1517
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 Db 1215 TCCCAGTGGGACCTGGGGCCTGAACTGCAATGAGACTTGCATCTGTGCCAATGGAGCTGC 1274

Qy 1518 CTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGGCGCGGGGAGAAATGCGA 1577
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 Db 1275 CTGCAGCCCCTTTGATGGGTCTGTGCCTGCACCCAGGCTGGCTGGGGGACTCCTGTGA 1334

Qy 1578 ACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAGCGCTGCGACTGCAGCCA 1637
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 Db 1335 ACTGCCCTGCCCGGACGGCATTGTTGGGTGAACTGCAGTGAAGCATTGCGACTGCAGCCA 1394

Qy 1638 CGCAGATGGCTGCCACCCTACCACGGGGCCATTGCCGCTGCCTCCCGGGATGGTCAGGTGT 1697
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 Db 1395 TGCTGATGGCTGTGACCCTGTCACAGGCCACTGCTGCTGCCTGGCAGGATGGACAGGCAT 1454

Qy 1698 CCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAACTGCTCCCTGCCCTGCTA 1757
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 Db 1455 CCGCTGTGATAGCACGTGTCTCCAGTCTGCTGGGGCCCCAACTGTTCAAGTGTCTGTCAG 1514

Qy 1758 CTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGCGAGTGTGCACCAGGCTT 1817
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Qy 1818 CCGAGGCACCACTTGTGAGAGGATCTGCTCCCCTGGTTTTATGGGCATCGCTGCAGCCA 1877
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Qy 1878 GACATGCCCACAGTGCCTTCACAGCAGCGGGGCCCTGCCACCACATCACCGGCCTGTGTGA 1937
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 Db 1635 GCCTTGTCCCCTCTGCGTGCACAGCAGGGGGCCCTGCCACCACATCAGTGGTATCTGTGA 1694

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Qy 2298 CTGCGACCACATTTCTGGGCAGTGTACTTGCCGCACTGGATTTCATGGGACGGCACTGTGA 2357
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 Db 2055 CTGTGACCACATCACTGGGAAATGCACCTGTGAACAGGCTTCTCTGGCCGCCACTGTGA 2114

Qy 2358 GCAGAAAGTCCCTTCAGGAACATATGGCTATGGCTGTGCCAGATATGTGATTGTCTGAA 2417

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Db      2115 ACAGAGATGTGCCCCTGGAACCTTTGGATATGGGTGTCAGCAGCTATGTGAGTGCATGAA 2174

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Qy      2478 GAGATGTGATCAAGCTGGTGTTCATCATAGTTGGAAATCTGAACAGCTTAAGCCGAACCAG 2537
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Qy      2538 TACTGCTCTCCCTGCTGATTCTTACCAGATCGGGGCCATTGCAGGCATCATCATTCTTGT 2597
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Qy      2598 CCTAGTTGTTCTCTTCTTCTACTGGCATTGTTTCATTATTTATAGACACAAGCAGAAGGGGAAA 2657
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Qy      2658 GGAATCAAGCATG---CCAGCAGTTACCTACACCCCTGCTATGAGGGTCGTCAATGCAGA 2714
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Db      2412 AGGCCGTGACCTGGCTCCCCGAGTCTCCTACACCCAGCCATGAGGATGACCAGCACAGA 2471

Qy      2715 TTATACCATTTTCAGGAAC 2732
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Db      2472 CTACTCTCTCTCAGGCAC 2489

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RESULT 5

AK032661

LOCUS AK032661 3466 bp mRNA linear HTC 18-SEP-2003

DEFINITION Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:6530404N23 product:MEGF11 PROTEIN (KIAA1781) homolog [Homo sapiens], full insert sequence.

ACCESSION AK032661

VERSION AK032661.1 GI:26082960

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3466)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/

URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .3466

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="FANTOM_DB:6530404N23"


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/db_xref="MGI:2396257"
/db_xref="taxon:10090"
/clone="6530404N23"
/tissue_type="cerebellum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="10 days neonate"
misc_feature 1. .3466
/note="MEGF11 PROTEIN (KIAA1781) homolog [Homo sapiens]
(SPTR|Q96KG6, evidence: FASTY, 85.9%ID, 85.4%length,
match=2363)"

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ORIGIN

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Query Match          26.1%;  Score 892.6;  DB 11;  Length 3466;
Best Local Similarity 69.1%;  Pred. No. 1.3e-243;
Matches 1219;  Conservative 0;  Mismatches 544;  Indels 0;  Gaps 0;

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Qy      94 AATGTGTGTAGCCACTGGGAAAGCTACTCAGTGACTGTGCAAGAGTCATACCCACATCCC 153
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Qy     154 TTTGATCAAATTTACTACACGAGCTGCACTGACATTCTAAACTGGTTTAAATGCACGCGG 213
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Db      61 TTTGATCAGATCTACTACACAGATGTGCAGACATCCTCAACTGGTTCAGTGTACCCGG 120

Qy     214 CACAGAGTCAGCTATCGGACAGCCTATCGACATGGGGAGAAGACTATGTATAGGCGCAAG 273
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Db     121 CACCGGATCAGCTATAAGACCGCGTATAGGCGCGGCCTCCGGACCATGTACCGGCGGAGG 180

Qy     274 TCTCAGTGTGTCTGCTGGATTTTATGAAAGCGGGGAAATGTGTGTCCCCACTGTGCTGAT 333
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Db     181 TCCAATGCTGCCCTGGCTACTATGAGAACGGAGACTTCTGCATTCCTCTGTGTACCGAG 240

Qy     334 AAATGTGTCCATGGTTCGCTGTATTGCTCCAAACACCTGTCAGTGTGAGCCTGGCTGGGGA 393
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Db     241 GAGTGCATGCACGGCCGCTGTGTCTCTCCGATACCTGCCACTGTGAGCCTGGATGGGGA 300

Qy     394 GGGACCAACTGCTCCAGTGCCTGCGATGGTGATCACTGGGGTCCCCACTGCACCAGCCGG 453
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Db     301 GGCCCTGACTGCTCCAGCGGCTGTGACAGCGAGCACTGGGGTCCCCACTGCAGCAACCGG 360

Qy     454 TGCCAGTGCAAAAATGGGGCTCTGTGCAACCCCATCACCGGGGCTTGCCACTGTGCTGCG 513
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Db	661	GAATGTGCCTGCCCTCCAGGCTGGACGGGAGCAGTGTGTGCCCAGCCCTGCCCTCCAGGG	720
Qy	814	CGCTTTGGAAAGAACTGTTCCCAAGAAATGCCAGTGCCATAATGGAGGGACGTGTGATGCT	873
Db	721	ACCTTTGGCCAGAAGTGTAGCCAGGACTGTCCCTGCCACCATGGAGGCCAGTGTGACCAT	780
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Qy	934	CCTGTTGGGACCTATGGCGTTCTCTGTGCTGAGACCTGCCAGTGTGTCAACGGAGGGAAG	993
Db	841	CCCTTTGGAACGTTTCGGTTTCCTGTGCTCTCAACGCTGTGACTGCCACAATGGAGGTCAA	900
Qy	994	TGTTACCACGTGAGCGGCGCATGCCCTCTGTGAAGCAGGCTTTGCTGGCGAGCGCTGCCGA	1053
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Db	1021	ACCGAGAACTATCAGCTGCCATCCAGTTACTGGAGCTGTACCTGCCAACCAGGCTGG	1080
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Qy	1234	ATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTGTGACTGGAAAGTGCACCTGTGCC	1293
Db	1141	CCCTGCACCTGCCAGAACGGTGTGACTGCCACAGTATACCGGGAGCTGCACTTGTGCT	1200
Qy	1294	CCAGGATTCAAAGGAATTGACTGCTCTACCCCATGCCCTCTGGGAACCTATGGGATAAAC	1353
Db	1201	CCAGGCTTCATGGGAGAGGTGTGTGCCGTCCCCTGTGCTGCAGGGACCTATGGTCCCAAC	1260
Qy	1354	TGTTCCCTCTCGCTGTGGCTGTAAAAATGATGCAGTCTGCTCTCCTGTGGACGGGTCTTGT	1413
Db	1261	TGTTTCATCTGTATGTAGCTGTAGCAACGGCGGCACCTGTCCCCAGTGGATGGCTCCTGC	1320
Qy	1414	ACTTGCAAGGCAGGCTGGCACGGGGTGGACTGCTCCATCAGATGTCCCAGTGGCACATGG	1473
Db	1321	ACCTGCCGAGAGGGATGGCAGGGCCTGGACTGCTCCCTGCCTTGTCCCAGTGGGACCTGG	1380
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Qy	1534	GGGACCTGCACGTGTGCACCTGGATGGCGCGGGGAGAAATGCGAACTTCCCTGCCAGGAT	1593

Db	1441	GGGTCCTGTGCCTGCACCCAGGCTGGCTGGGGGACTCCTGTGAACCTGCCCTGCCCGGAC	1500
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Db	1561	CCTGTACACAGGCCACTGCTGCTGCCTGGCAGGATGGACAGGCATCCGCTGTGATAGCACG	1620
Qy	1714	TGTGCTGAGGGACGCTGGGGCCCCAACTGCTCCCTGCCCTGCTACTGTAAAAATGGGGCT	1773
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Qy	1774	TCATGCTCCCCTGATGATGGCATCTGCGAGTGTGCACCAGGCTTCCGAGGCACCACTTGT	1833
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Qy	1834	CAGAGGATCTGCTCCCCTGGTTT	1856
Db	1741	CAGAGAAGTAAGGCTCCTGATTT	1763

RESULT 6

AY406555

LOCUS	AY406555	2910 bp	DNA	linear	GSS 12-DEC-2003
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DEFINITION Pan troglodytes HCM2596 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY406555

VERSION AY406555.1 GI:39762526

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 2910)

AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2910)

AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES	Location/Qualifiers
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source      1. .2910

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/organism="Pan troglodytes"
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Qy	1158	CTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGTTCTCCTGGATTCTACGG	1217
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Qy	1218	GGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTGTGACTGG	1277
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Db	1515	CTGTGAGAATGGAGGCTCCTGCTCCCAGAGGATGGGAGCTGCGAGTGTGCCCTGGCTT	1574
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[illegible]

Db || |
2472 CTACNNNNNNNNNG 2486

RESULT 7

AK053551

LOCUS AK053551 3556 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130107B17 product:similar to MEGF12 [Mus musculus], full insert sequence.

ACCESSION AK053551

VERSION AK053551.1 GI:26343538

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,

Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .3556
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:E130107B17"
/db_xref="MGI:2425343"
/db_xref="taxon:10090"
/clone="E130107B17"
/tissue_type="eyeball"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
CDS 205. .3309

/note="unnamed protein product; putative similar to MEGF12 [Mus musculus] (SPTR|AAL33583, evidence: FASTY, 72.7%ID, 41.5%length, match=1604)"
/codon_start=1
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FSLLPAESCHRPWEDPHTCAQPTVVYRTVYRQVVKMDSRPRLQCCRGYYESRGACVPL
CAQECVHGRCVAPNQCCAPGWRGGDCSSECAPGMWGPQCDKFCHCGNNSCDPKSGT
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SQGTDGFFCPRTPYPCQNGGVPQGSQGSQSCSPPGWMGVICSLPCEGFHGPNECTQECRC
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EHGFTGDRCTERLCPDGRYGLSCQEPCTCDPEHSLSCHPMHGECSQPGWAGLHCNES
CPQDTHGPGCQEHCLCLHGGLCLADSGLCRCAPGYTGPHCANLCPDPTYGINCSSRCS
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CTPGWHGAHCQLPCPKGQFGEGCASVCDCHSDGCDPVHGGQCRCQAGWMGTRCHLPCP
EGFWGANCSNTCTCKNGGTCVSENGNCVCAPGFRGPSCQRPCPPGRYKRCVQCKCNN

Qy	731	GAGTGTGTGCATCACGTCACTGGAGAAATGCTCTTGGCCCTTCTGGCTGGATGGGCACAGTGT	790
Db	914	GTGTTTCCTCAGGGGCTCCCAAGGCTCCTGCAGCTGCCACCGGGCTGGATGGGTGTCATTT	973
Qy	791	GTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAATGCCAGTGCC	850
Db	974	GTTCCCTGCCATGCCAGAGGGTTTCCATGGACCCAAGTGTACTCAGGAATGTCGCTGCC	1033
Qy	851	ATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCAGGATACACAG	910
Db	1034	ACAACGGTGGCCTCTGTGACAGGTTTACTGGGCAGTGCCACTGTGCTCCTGGCTATATCG	1093
Qy	911	GGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGTGCTGAGACCT	970
Db	1094	GGGATCGGTGCCAAGAAGAGTGCCCCGTGGGCCGCTTCGGTCAAGACTGTGCTGAGACCT	1153
Qy	971	GCCAGTGTGTCAACGGAGGGAAGTGTACCACGTGAGCGGCGCATGCCTCTGTGAAGCAG	1030
Db	1154	GTGACTGTGCTCCTGGCGCCCGTTGCTTTCCTGCTAATGGCGCGTGTCTGTGTGAACATG	1213
Qy	1031	GCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCTGAGGGGCTCTACGGCATCAAAT	1090
Db	1214	GCTTCACAGGCGACCGCTGCACTGAGCGCCTCTGTCCGGATGGCCGCTATGGTCTGAGCT	1273
Qy	1091	GTGACAAACGGTGTCCCTGCCACTTGAAAAACACTCATAGCTGTACCCCATGTCTGGAG	1150
Db	1274	GCCAGGAGCCCTGCACCTGCGACCCAGAACACAGTCTCAGCTGCCACCCGATGCACGGCG	1333
Qy	1151	AGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGTTCTCCTGGAT	1210
Db	1334	AGTGCTCCTGCCAGCCAGGTTGGGCGGGCCTCCACTGCAACGAGAGCTGCCCTCAGGACA	1393
Qy	1211	TCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTG	1270
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Qy	1271	TGACTGGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACCCCATGCC	1330
Db	1454	ACAGCGGCCTCTGCCGGTGC GCGCCGGGATACACGGGACCTCACTGCGCTAACCTATGTC	1513
Qy	1331	CTCTGGGAACCTATGGGATAAACTGTTCCCTCTCGCTGTGGCTGTAAAAATGATGCAGTCT	1390
Db	1514	CACCGGACACTTACGGGATCAACTGTTCCCTCCGCTGCTCCTGTGAAAATGCCATTGCCT	1573
Qy	1391	GCTCTCCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCACGGGGTGGACTGCTCCA	1450
Db	1574	GCTCTCCCATCGACGGCACGTGCATCTGCAAGGAAGGTTGGCAGCGTGGTAACTGCTCTG	1633
Qy	1451	TCAGATGTCCCAAGTGGCACATGGGGCTTTGGCTGTAACCTTAACATGCCAGTGCCTCAACG	1510
Db	1634	TTCCCTGTCCCTTGGCACCTGGGGCTTCAATTGCAATGCCAGTTGCCAGTGTGCCACG	1693
Qy	1511	GGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGGCGCGGGGAGA	1570
Db	1694	ACGGAGTCTGCAGCCCCCAAAGTGGAGCCTGTACTTGCACCCCTGGGTGGCATGGTGCTC	1753

Qy	1571	AATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAGCGCTGCGACT	1630
Db	1754	ACTGCCAGCTTCCCTGCCCCAAGGGACAGTTTGGTGAAGGCTGTGCCAGTGTCTGTGACT	1813
Qy	1631	GCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTCCCGGGATGGT	1690
Db	1814	GTGACCACTCTGATGGCTGTGACCCTGTTTCATGGACAGTGCCGATGTCAGGCTGGTTGGA	1873
Qy	1691	CAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAACTGCTCCCTGC	1750
Db	1874	TGGGCACACGCTGCCACCTGCCTTGCCCGAGGGCTTTTGGGGAGCCAACTGCAGTAACA	1933
Qy	1751	CCTGCTACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGCGAGTGTGCAC	1810
Db	1934	CCTGTACCTGCAAGAATGGTGGTACCTGTGTGTCTGAGAATGGCAACTGCGTGTGCGCAC	1993
Qy	1811	CAGGCTTCCGAGGCACCACTTGTGAGAGGATCTGCTCCCCTGGTTTTTATGGGCATCGCT	1870
Db	1994	CAGGGTTCCGAGGCCCCCTCCTGCCAGAGGCCCTGCCCGCCTGGTCGCTATGGCAAACGCT	2053
Qy	1871	GCAGCCAGACATGCCACAGTGCGTTTACAGCAGCGGGCCCTGCCACCACATCACCGGCC	1930
Db	2054	GTGTGCA-----ATGCAAGTGTAACAACAACCATTCTTCCTGCCACCCATCGGACGGGA	2107
Qy	1931	TGTGTGACTGCTTGCTGGCTTACAGGCGCCCTCTGCAATGAAGTGTGTCCCAGTGGCA	1990
Db	2108	CCTGCTCCTGCCTGGCGGGCTGGACAGGCCCTGACTGCTCCGAGGCATGTCCCCAGGCC	2167
Qy	1991	GATTTGGGAAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACCTGTAACCCCA	2050
Db	2168	ACTGGGACTCAAATGCTCCCAACTCTGCCAGTGTCTCATGCTGGTGGGACCTGCCACCCCC	2227
Qy	2051	TTGACAGATCTTGTGAGTGTACCCCGGTTGGATTGGCAGTGACTGCTCTCAACCATGTC	2110
Db	2228	AGGATGGGAGCTGTATCTGCACGCCAGGCTGGACTGGACCCAAGTCTTGAAGGCTGCC	2287
Qy	2111	CACCTGCCCCTGGGGCCCCAACTGCATCCACACGTGCAACTGCCATAATGGAGCTTTCT	2170
Db	2288	CACCAAGAATGTTTGGTGTCAACTGCTCCCAGCTATGTGAGTGTGATCTCGGAGAGATGT	2347
Qy	2171	GCAGCGCCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTCTACTGCACTC	2230
Db	2348	GCCACCCAGAGACTGGGGCTTGTGTCTGTCCCCCAGGACACAGTGGTGCAGACTGCAAAA	2407
Qy	2231	AGAGATGTC	2239
Db	2408	TGGGAAGCC	2416

RESULT 8

CD803668

LOCUS CD803668 789 bp mRNA linear EST 15-JUL-2003

DEFINITION UI-M-GV0-chv-b-08-0-UI.r1 NIH_BMAP_GV0 Mus musculus cDNA clone
IMAGE:30544831 5', mRNA sequence.

ACCESSION CD803668

VERSION CD803668.1 GI:32462494

KEYWORDS EST.

VERSION BU215784.1 GI:25394329
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 921)
 AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
 TITLE A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 22335534
 PUBMED 12445392
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 FEATURES Location/Qualifiers
 source 1. .921
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, Hisex"
 /db_xref="taxon:9031"
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 /note="Organ: whole embryo; Vector: pBluescript II KS(+);
 Site_1: EcoRI; Site_2: NotI; This normalized library was
 constructed from 1 million independent clones. cDNA
 synthesis was initiated using an oligo(dT) primer, using
 methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunted, ligated to NotI adapters, digested with
 EcoRI, size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."
 ORIGIN
 Query Match 15.7%; Score 539; DB 13; Length 921;
 Best Local Similarity 75.6%; Pred. No. 1.7e-142;
 Matches 695; Conservative 0; Mismatches 220; Indels 4; Gaps 2;
 Qy 787 GTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGAAAGAACTGTTCCCAAGAATGCCAG 846
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QY	847	TGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCAGGATAC	906
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QY	907	ACAGGGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGTGCTGAG	966
Db	123	ACAGGAGAACGCTGTCAAGATGAGTGTCCAGTGGGCACTTACGGAGTACGGTGTGCTGAG	182
QY	967	ACCTGCCAGTGTGTCAACGGAGGGAAGTGTACCACGTGAGCGGCGCATGCCTCTGTGAA	1026
Db	183	ACCTGCCAGTGTATGAATGGTGGGAAATGCTACCATATCAGCGGTGCTTGCCTCTGTGAA	242
QY	1027	GCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCTTGAGGGGCTCTACGGCATC	1086
Db	243	CCAGGATATACTGGAGAGCAC'TGTGAAACAAGGCTTTGCCCTGAGGGGGT'TTATGGTCTC	302
QY	1087	AAATGTGACAAACGGTGTCCCTGCCACTTGGAAAACTCATAGCTGTCACCCCATGTCT	1146
Db	303	AAATGTGACAAAAGTGTCCCTGCCACTTGCATAATACCTGGAGCTGTCACCCTATGTCT	362
QY	1147	GGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGTTCTCCT	1206
Db	363	GGGGAATGCTCCTGCAAGCCCGGCTGGTCTGGGCTCTACTGCAACGAGACATGTTCTCCG	422
QY	1207	GGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGAC	1266
Db	423	GGGTTCTACGGCAAGTCTTGT CAGCAGATTTCAGCTGCCAAAATGGTGCTGACTGTGAC	482
QY	1267	AGTGTGACTGGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACCCCA	1326
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QY	1327	TGCCCTCTGGGAACCTATGGGATAAACTGTTCCCTCTCGCTGTGGCTGTAAAAATGATGCA	1386
Db	543	TGTCTTCCGGGTACATATGGAGTAAATTGTTCTTCTGTCTGCAACTGTAAAAACGAAGCC	602
QY	1387	GTCTGCTCTCCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCACGGGGTGGACTGC	1446
Db	603	ATCTGTT CATCAGTAGATGGTTC'TGTACCTGCAAAGCAGGT'TGGCATGGTGTAGACTGT	662
QY	1447	TCCATCAGATGTCCAGTGGCACATGGGGCTTTGGCTGTAACTTAACATGCCAGTGCCTC	1506
Db	663	TCAATCAATTGTCCCAGCGGTACCTGGGGACTTGGCTGCAACTTAAC TTGCCAGTGTCTT	722
QY	1507	AACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGGCGCGGG	1566
Db	723	AACGGAGGGGCTTGCAATGCTCTAGATGGAACCTGTACCTGCGCTCCGGGCTGGAGAGGA	782
QY	1567	GAGAAATGCGAACTTCCCT--GCCAGGATGGCACGTACGGGCTGAACTGTGCTGAGCGCT	1624
Db	783	GAGAACGTGTGAACTCCCTTGGCCAGGACGGTACCTATGGCATGGATTGTGCTGAGCGCT	842
QY	1625	GCG--ACT'GCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTCCC	1682
Db	843	GTGGACCTGCAGCATGCAGATGGGTTGT CATCCTACCACGGGTTACTGTCCCTGTCTACC	902
QY	1683	GGGATGGTCAAGTGTCCAC	1701

Db | | | | | | |
903 AGATGGTCCGGTTTCCCTC 921

RESULT 10

CD802967

LOCUS CD802967 755 bp mRNA linear EST 15-JUL-2003

DEFINITION UI-M-GV0-ch1-j-22-0-UI.r1 NIH_BMAP_GV0 Mus musculus cDNA clone
IMAGE:30543885 5', mRNA sequence.

ACCESSION CD802967

VERSION CD802967.1 GI:32461793

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 755)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>

This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pYX-5.

FEATURES

source

Location/Qualifiers

1. .755

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:30543885"

/tissue_type="whole brain"

/dev_stage="1,5, and 15 days newborn"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH_BMAP_GV0"

/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;

Site_2: Not I; The library was constructed according

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction, ligated with

EcoR I adaptor, digested with NotI and then cloned

directionally into pYX-Asc vector. The library tag

sequence located between the Not I site and the polyA tail

is CGAACTGAAT. This library was created for the University

Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the

Developing Mouse Nervous System', supported by National

Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,

program coordinator."

ORIGIN

Query Match 15.5%; Score 530.4; DB 14; Length 755;
 Best Local Similarity 84.5%; Pred. No. 4.4e-140;
 Matches 594; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

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Qy      61 GGGACAGCATCACCTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTAC 120
      |||||  |||||  |  |||||  ||  |||||  ||  ||  ||  |||||  |||||  |||||
Db      112 GGGACAGCATCCTCCCTGAACCTGGAAGACCCCAACGTATGCAGCCACTGGGAAAGCTAC 171

Qy      121 TCAGTGA CTGTGCAAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGC 180
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Db      232 ACCGACATCCTGAACCTGGTTTAAATGCACACGCGGCACAGAATCAGCTACCGGACAGCCTAC 291

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Qy      301 AGCGGGGAAATGTGTGTCCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTGCT 360
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Qy      361 CCAAACACCTGTCACTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGAT 420
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Db      532 AACCCCATCACCGGTGCTTGCCACTGCGCTGCGGGCTACCGGGGATGGCGCTGCGAGGAC 591

Qy      541 CGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATGGA 600
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Qy      601 GCCACCTGCGACCACGTACGCGGGGAATGCCGCTGCCCACCAGGATACACCGGAGCCTTC 660
      ||  |||||  |||||  |||||  |||||  |||||  ||  |||||  |||||  |||||
Db      652 GCGACCTGTGACCACATCACTGGGGAATGCCGTTGTTACCTGNGTACACTNGGAGCTTC 711

Qy      661 TGTGAGGATCTTTGTCTCCTGGTAAACATGGTCCACAGTGTG 703
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LOCUS BU056532 643 bp mRNA linear EST 26-AUG-2002
 DEFINITION UI-M-FO0-cab-n-24-0-UI.r1 NIH_BMAP_F00 Mus musculus cDNA clone
 IMAGE:6409175 5', mRNA sequence.
 ACCESSION BU056532
 VERSION BU056532.1 GI:22496609
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 643)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: pYX-5.
 FEATURES Location/Qualifiers
 source 1. .643
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:6409175"
 /tissue_type="whole brain"
 /dev_stage="embryo 12.5dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_F00"
 /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
 Site_2: Not I; The library was constructed according
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is TGAGAGAGCC. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."
 ORIGIN
 Query Match 14.9%; Score 508.6; DB 13; Length 643;
 Best Local Similarity 86.9%; Pred. No. 7.2e-134;
 Matches 559; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

- Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
- REFERENCE 1
 AUTHORS Carninci,P. and Hayashizaki,Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
- REFERENCE 2
 AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
- REFERENCE 3
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
- REFERENCE 4
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
- REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
- REFERENCE 6 (bases 1 to 2944)
 AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers
source 1. .2944
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:C230074H09"
/db_xref="MGI:2415973"
/db_xref="taxon:10090"
/clone="C230074H09"
/tissue_type="cerebellum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
CDS 154..1053
/note="unnamed protein product; MEGF11 PROTEIN (KIAA1781)
homolog [Homo sapiens] (SPTR|Q96KG6, evidence: FASTY,
85.9%ID, 85.4%length, match=2363)
putative"
/codon_start=1
/protein_id="BAC33471.1"
/db_xref="GI:26339600"
/translation="MAPSAVGLLVFLQAAALALNPEDPNVCSHWESYAVTVQESYAHF
FDQIYYTRCADILNWFKCTRHRISYKTAYRRGLRTMYRRRSQCCPGYYENGDFCIPLC
TEECMHGRCVSPDTCHEPGWGGPDCSSGCDSEHWGPHCSNRCQCQNGALCNPITGAC
VCAPGFRGWRCEELCAPGTHGKGCQLLCQCHHGASCDPRTGECCLCAPGYTGVYCEELC
PPGSHGAHCELRCPCQNGGTCHHITGECACPPGWTGAVCAQPCPPGTFGQNCSDCPC
HHGGQCDHVTGQCHCTAGYMGDR"

ORIGIN

Query Match 13.7%; Score 470; DB 11; Length 2944;
Best Local Similarity 72.2%; Pred. No. 2.3e-122;
Matches 611; Conservative 0; Mismatches 235; Indels 0; Gaps 0;

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Qy      74 CTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTACTCAGTGACTGTGC 133
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Db      206 CTCTGAACCCTGAAGACCCCAATGTGTGTAGCCACTGGGAGAGCTATGCCGTGACTGTGC 265

Qy      134 AAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGCACTGACATTCTAA 193
      | |||| | | ||| ||||| | ||||| | ||||| | ||| | ||||| | |
Db      266 AGGAGTCTTATGCACACCCCTTTGATCAGATCTACTACACACGATGTGCAGACATCCTCA 325

Qy      194 ACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCTATCGACATGGGGAGA 253
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Db      326 ACTGGTTCAAGTGTACCCGGCACCGGATCAGCTATAAGACCGCGTATAGGCGCGGCCTCC 385

Qy      254 AGACTATGTATAGGCGCAAGTCTCAGTGTGTCTCTGGATTTTATGAAAGCGGGGAAATGT 313
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Db	386	GGACCATGTACCGGCGGAGGTCCCAATGCTGCCCTGGCTACTATGAGAACGGAGACTTCT	445
Qy	314	GTGTCCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTGCTCCAAACACCTGTC	373
Db	446	GCATTCTCTGTGTACCGAGGAGTGCATGCACGGCCGCTGTGTCTCTCCCGATACCTGCC	505
Qy	374	AGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGATGGTGATCACTGGG	433
Db	506	ACTGTGAGCCTGGATGGGGAGGCCCTGACTGCTCCAGCGGCTGTGACAGCGAGCACTGGG	565
Qy	434	GTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGCAACCCCATCACCG	493
Db	566	GTCCCCACTGCAGCAACCGGTGTCAGTGTGACAACGGCGCCCTGTGCAACCCATCACCG	625
Qy	494	GGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGACCGCTGTGAGCAGG	553
Db	626	GCGCCTGCGTGTGCGCCCCGGGCTTCCGAGGCTGGCGCTGTGAGGAACCTCTGCGCTCCTG	685
Qy	554	GCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATGGAGCCACCTGCGACC	613
Db	686	GTACTCACGGCAAGGGCTGCCAGCTGCTCTGTGAGTGCCACCATGGCGCCAGCTGTGACC	745
Qy	614	ACGTCACGGGGGAATGCCGCTGCCCACCAGGATACACCGAGCCTTCTGTGAGGATCTTT	673
Db	746	CGCGCACTGGCGAGTGCCTCTGCGCTCCTGGCTACACAGGCGTTTACTGTGAGGAGCTGT	805
Qy	674	GTCCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGTCAAAATGGAGGAG	733
Db	806	GCCCCCTGGGAGCCATGGAGCTCACTGTGAGCTGCGCTGCCCCTGCCAGAATGGAGGCA	865
Qy	734	TGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGATGGGCACAGTGTGTG	793
Db	866	CCTGCCACCACATCACTGGCGAATGTGCCTGCCCTCCAGGCTGGACGGGAGCAGTGTGTG	925
Qy	794	GTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAATGCCAGTGCCATA	853
Db	926	CCCAGCCCTGCCCTCCAGGACCTTTGGCCAGAAGTGTAGCCAGGACTGTCCCTGCCACC	985
Qy	854	ATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCAGGATACACAGGGG	913
Db	986	ATGGAGGCCAGTGTGACCATGTGACTGGACAATGCCACTGTACAGCTGGATACATGGGGG	1045
Qy	914	AACGGT	919
Db	1046	ACAGGT	1051

RESULT 13

BG828819

LOCUS BG828819 755 bp mRNA linear EST 22-MAY-2001

DEFINITION 602751395F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4904255 5', mRNA sequence.

ACCESSION BG828819

VERSION BG828819.1 GI:14176418

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 755)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1803 row: m column: 24
High quality sequence stop: 707.

FEATURES
source Location/Qualifiers
1. .755
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4904255"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_17"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 13.3%; Score 456.6; DB 12; Length 755;
Best Local Similarity 98.8%; Pred. No. 6.7e-119;
Matches 481; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

Qy 1 ATGGTTATTTCTTTGAACTCATGCCTGAGCTTTATTTGTTTATTGTTATGCCACTGGATT 60
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Db 268 ATGGTTATTTCTTTGAACTCATGCCTGAGCTTTATTTGTTTATTGTTATGCCACTGGATT 327

Qy 61 GGGACAGCATCACCTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTAC 120
|||||
Db 328 GGGACAGCATCACCTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTAC 387

Qy 121 TCAGTGACTGTGCAAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGC 180
|||||
Db 388 TCAGTGACTGTGCAAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGC 447

Qy 181 ACTGACATTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCTAT 240
|||||
Db 448 ACTGACATTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCTAT 507

Qy 241 CGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTGTCCTGGATTTTATGAA 300
 |||
 Db 508 CGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTGTCCTGGATTTTATGAA 567
 Qy 301 AGCGGGGAAATGTGTGTCCCCCACTGTGCTGATAAATGTGTCCATGGTC-GCTGTATTGC 359
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 Db 568 AGCGGGGAAATGTGTGTCCCCCACTGTGCTGATAAATGTGTCCATGGTCGGCTGTATTGC 627
 Qy 360 TCCAAACACCTGTCACTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCCA 419
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 Db 628 TCCAAACACCTGTCACTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCCA 687
 Qy 420 TGGTGATCACTGGGGTCCCCACTGCACCAGCCGGTG-CCAGTGCAAAAATGGGGCTCTGT 478
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 Db 688 TGGTGATCACTGGAGTCCCAATGCACCAGCCGGTGCCCAGTGCAAACATGGGGCTCTGT 747
 Qy 479 GCAACCC 485
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 Db 748 GCCACCC 754

RESULT 14

BM719978

LOCUS BM719978 565 bp mRNA linear EST 01-MAR-2002

DEFINITION UI-E-EJ0-ahu-i-16-0-UI.r1 UI-E-EJ0 Homo sapiens cDNA clone
 UI-E-EJ0-ahu-i-16-0-UI 5', mRNA sequence.

ACCESSION BM719978

VERSION BM719978.1 GI:19038910

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 565)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa

DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa

Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).

Seq primer: M13 Reverse.

FEATURES Location/Qualifiers

source 1. .565

/organism="Homo sapiens"


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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJ0-ahu-i-16-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ0"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJ0 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment,
AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI)."
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ORIGIN

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Query Match          12.6%;  Score 433;  DB 12;  Length 565;
Best Local Similarity 100.0%;  Pred. No. 3.3e-112;
Matches 433;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy      2800 ACCCAGTGTGCCACATCCCCTCACGTCAACAACAGGGACAGGATGACTGTCACGAAGTCA 2859
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Db        1 ACCCAGTGTGCCACATCCCCTCACGTCAACAACAGGGACAGGATGACTGTCACGAAGTCA 60

Qy      2860 AAAAACAATCAACTGTTTGTGAATCTTAAAAATGTGAACCCTGGGAAGAGAGGCCCTGTG 2919
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Db        61 AAAAACAATCAACTGTTTGTGAATCTTAAAAATGTGAACCCTGGGAAGAGAGGCCCTGTG 120

Qy      2920 GGGGACTGCACTGGGACATTGCCGGCTGACTGGAAACATGGCGGCTACCTCAACGAGCTC 2979
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Db       121 GGGGACTGCACTGGGACATTGCCGGCTGACTGGAAACATGGCGGCTACCTCAACGAGCTC 180

Qy      2980 GGTGCTTTTGGACTTGACAGAAGCTATATGGGAAAATCCTTAAAAGACCTGGGAAAGAAT 3039
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Qy      3040 TCTGAATATAATTCAAGTAACTGCTCCCTAAGCAGTTCTGAGAACCCATATGCCACTATT 3099
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Db       241 TCTGAATATAATTCAAGTAACTGCTCCCTAAGCAGTTCTGAGAACCCATATGCCACTATT 300

Qy      3100 AAAGACCCACCTGTACTTATCCCGAAAAGCTCAGAGTGTGGTTATGTGGAGATGAAATCG 3159
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Db       301 AAAGACCCACCTGTACTTATCCCGAAAAGCTCAGAGTGTGGTTATGTGGAGATGAAATCG 360

Qy      3160 CCGGCACGAAGAGATTCCCATATGCAGAGATCAATAACTCAACTTCAGCCAACAGGAAT 3219
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Db      361 CCGGCACGAAGAGATTCCCCATATGCAGAGATCAATAACTCAACTTCAGCCAACAGGAAT 420
Qy      3220 GTCTATGAAGTTG 3232
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Db      421 GTCTATGAAGTTG 433

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RESULT 15

BM676825/c

LOCUS BM676825 598 bp mRNA linear EST 27-FEB-2002

DEFINITION UI-E-EJ0-ahu-i-16-0-UI.s2 UI-E-EJ0 Homo sapiens cDNA clone

UI-E-EJ0-ahu-i-16-0-UI 3', mRNA sequence.

ACCESSION BM676825

VERSION BM676825.1 GI:18986721

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 598)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa

DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa

Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).

Seq primer: M13 Forward

POLYA=Yes.

FEATURES

source

Location/Qualifiers

1. .598

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-E-EJ0-ahu-i-16-0-UI"

/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"

/dev_stage="fetal and adult"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone_lib="UI-E-EJ0"

/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;

UI-E-EJ0 is a subtracted cDNA library constructed

according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
TAG_TISSUE=human fetal eyes
TAG_LIB=UI-E-EJ0
TAG_SEQ=AGAATCAAGA"

ORIGIN

Query Match 12.6%; Score 432; DB 12; Length 598;
Best Local Similarity 98.9%; Pred. No. 6.6e-112;
Matches 435; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy      2793 CACGCTCACCCAGTGTGCCACATCCCCTCACGTCAACAACAGGGACAGGATGACTGTCAC 2852
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Db      596 CACGAGGACCCAGTGTGCCACATCCCCTCACGTCAACAACAGGGACAGGATGACTGTCAC 537

Qy      2853 GAAGTCAAAAAACAATCAACTGTTTGTGAATCTTAAAAATGTGAACCCTGGGAAGAGAGG 2912
          ||||||||||||||||||||||||||||||||||||||||||||
Db      536 GAAGTCAAAAAACAATCAACTGTTTGTGAATCTTAAAAATGTGAACCCTGGGAAGAGAGG 477

Qy      2913 CCCTGTGGGGGACTGCACTGGGACATTGCCGGCTGACTGGAAACATGGCGGCTACCTCAA 2972
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Db      476 CCCTGTGGGGGACTGCACTGGGACATTGCCGGCTGACTGGAAACATGGCGGCTACCTCAA 417

Qy      2973 CGAGCTCGGTGCTTTTGGACTTGACAGAAGCTATATGGGAAAATCCTTAAAGACCTGGG 3032
          ||||||||||||||||||||||||||||||||||||||||||||
Db      416 CGAGCTCGGTGCTTTTGGACTTGACAGAAGCTATATGGGAAAATCCTTAAAGACCTGGG 357

Qy      3033 AAAGAATTCTGAATATAATTCAAGTAACTGCTCCCTAAGCAGTTCTGAGAACCCATATGC 3092
          ||||||||||||||||||||||||||||||||||||||||||||
Db      356 AAAGAATTCTGAATATAATTCAAGTAACTGCTCCCTAAGCAGTTTCTGAGAACCCATATGC 297

Qy      3093 CACTATTAAAGACCCACCTGTACTTATCCCGAAAAGCTCAGAGTGTGGTTATGTGGAGAT 3152
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Qy      3153 GAAATCGCCGGCACGAAGAGATTCCCCATATGCAGAGATCAATAACTCAACTTCAGCCAA 3212
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Qy      3213 CAGGAATGTCTATGAAGTTG 3232
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Db      176 CAGGAATGTTTATGAAGTTG 157

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Search completed: March 30, 2004, 08:33:24
Job time : 8353 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 30, 2004, 01:07:41 ; Search time 13015 Seconds
(without alignments)
11399.401 Million cell updates/sec

Title: US-10-092-390-1
Perfect score: 3423
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_ba:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8						
Result	Query					
No.	Score	Match	Length	DB	ID	Description
1	3421.4	100.0	7522	6	BD185216	BD185216 Novel gen
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3	2274.8	66.5	2952	9	AK123568	AK123568 Homo sapi
4	1692.4	49.4	2267	9	BC020198	BC020198 Homo sapi
5	1425.8	41.7	1448	6	AR217554	AR217554 Sequence
6	1425.8	41.7	1448	6	BD080296	BD080296 Tango-71,
7	1200.6	35.1	5702	9	AB058677	AB058677 Homo sapi
8	1040.8	30.4	5278	10	AK122555	AK122555 Mus muscu
9	742	21.7	3281	9	HSM805375	AL834326 Homo sapi
10	649.4	19.0	4290	10	AF444274	AF444274 Mus muscu
11	648.6	18.9	4539	10	AF461685	AF461685 Mus muscu
12	646.2	18.9	4482	10	AF440279	AF440279 Mus muscu
13	600.6	17.5	3574	6	AX492979	AX492979 Sequence
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15	534.8	15.6	632	6	AX079681	AX079681 Sequence
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17	456.8	13.3	4470	9	AK074121	AK074121 Homo sapi
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19	396.8	11.6	7334	6	AX817303	AX817303 Sequence
20	393	11.5	4835	6	AX817305	AX817305 Sequence
21	387	11.3	5178	6	AX704753	AX704753 Sequence
22	386.8	11.3	4733	6	AX817299	AX817299 Sequence
23	383.8	11.2	7319	6	AX817297	AX817297 Sequence
24	383.8	11.2	7337	6	AX817295	AX817295 Sequence
25	365.4	10.7	3391	10	BC031402	BC031402 Mus muscu
26	365.4	10.7	3402	10	BC039980	BC039980 Mus muscu
27	362.8	10.6	2629	10	BC058571	BC058571 Mus muscu
28	354.8	10.4	4501	9	AB011539	AB011539 Homo sapi
c 29	250.8	7.3	146206	9	AC026800	AC026800 Homo sapi
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c 31	250.8	7.3	175144	2	AC010415	AC010415 Homo sapi
c 32	250.8	7.3	217221	9	AC008682	AC008682 Homo sapi
c 33	243	7.1	48202	2	AC012911	AC012911 Drosophil

	34	243	7.1	172175	3	AC010038	AC010038	Drosophil
c	35	243	7.1	177583	3	AC105264	AC105264	Drosophil
c	36	243	7.1	257867	3	AC005557	AC005557	Drosophil
c	37	243	7.1	303191	3	AE003472	AE003472	Drosophil
	38	241.8	7.1	192282	9	AC010424	AC010424	Homo sapi
	39	239.8	7.0	2054	9	AK098809	AK098809	Homo sapi
	40	216	6.3	3764	3	AF332568	AF332568	Caenorhab
	41	197.2	5.8	185768	10	AC102173	AC102173	Mus muscu
c	42	192.4	5.6	194593	2	AC139989	AC139989	Rattus no
	43	192.4	5.6	226956	10	AC095558	AC095558	Rattus no
	44	192.4	5.6	231950	2	AC094759	AC094759	Rattus no
c	45	180	5.3	209476	2	AC122117	AC122117	Mus muscu

ALIGNMENTS

RESULT 1

BD185216

LOCUS BD185216 7522 bp DNA linear PAT 17-JUN-2003

DEFINITION Novel genes and proteins encoded by the genes.

ACCESSION BD185216

VERSION BD185216.1 GI:31877416

KEYWORDS JP 2002345493-A/59.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 7522)

AUTHORS Ohara,O., Nagase,T. and Nakajima,D.

TITLE Novel genes and proteins encoded by the genes

JOURNAL Patent: JP 2002345493-A 59 03-DEC-2002;

KAZUSA DNA RESEARCH INSTITUTE

COMMENT OS Homo sapiens (human)

PN JP 2002345493-A/59

PD 03-DEC-2002

PF 26-FEB-2002 JP 2002049046

PI OSAMU OHARA,TAKAHIRO NAGASE,DAISUKE NAKAJIMA

PC C12N15/09,C07K14/47,C07K14/54,C12N15/00

CC Novel genes and proteins encoded by the genes FH Key

Location/Qualifiers

FT CDS (48)..(3623).

FEATURES Location/Qualifiers

source 1..7522

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 3421.4; DB 6; Length 7522;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGTTATTTCTTTGAACTCATGCCTGAGCTTTATTTGTTTATTGTTATGCCACTGGATT 60

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Db 204 ATGGTTATTTCTTTGAACTCATGCCTGAGCTTTATTTGTTTATTGTTATGCCACTGGATT 263

Qy	61	GGGACAGCATCACCTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTAC	120
Db	264	GGGACAGCATCACCTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTAC	323
Qy	121	TCAGTGACTGTGCAAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGC	180
Db	324	TCAGTGACTGTGCAAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGC	383
Qy	181	ACTGACATTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCTAT	240
Db	384	ACTGACATTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCTAT	443
Qy	241	CGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTGTCCTGGATTTTATGAA	300
Db	444	CGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTGTCCTGGATTTTATGAA	503
Qy	301	AGCGGGGAAATGTGTGTCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTGCT	360
Db	504	AGCGGGGAAATGTGTGTCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTGCT	563
Qy	361	CCAAACACCTGTCAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGAT	420
Db	564	CCAAACACCTGTCAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGAT	623
Qy	421	GGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGC	480
Db	624	GGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGC	683
Qy	481	AACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGAC	540
Db	684	AACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGAC	743
Qy	541	CGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATGGA	600
Db	744	CGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATGGA	803
Qy	601	GCCACCTGCGACCACGTACGGGGGAATGCCGCTGCCCACCAGGATACACCGGAGCCTTC	660
Db	804	GCCACCTGCGACCACGTACGGGGGAATGCCGCTGCCCACCAGGATACACCGGAGCCTTC	863
Qy	661	TGTGAGGATCTTTGTCCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGT	720
Db	864	TGTGAGGATCTTTGTCCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGT	923
Qy	721	CAAAATGGAGGAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGATG	780
Db	924	CAAAATGGAGGAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGATG	983
Qy	781	GGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAA	840
Db	984	GGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAA	1043
Qy	841	TGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCA	900
Db	1044	TGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCA	1103
Qy	901	GGATACACAGGGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGT	960

Db	1104	 GGATACACAGGGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGT	1163
Qy	961	GCTGAGACCTGCCAGTGTGTCAACGGAGGGAAGTGTTACCACGTGAGCGGCGCATGCCTC	1020
Db	1164	 GCTGAGACCTGCCAGTGTGTCAACGGAGGGAAGTGTTACCACGTGAGCGGCGCATGCCTC	1223
Qy	1021	TGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCTGAGGGGCTCTAC	1080
Db	1224	 TGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCTGAGGGGCTCTAC	1283
Qy	1081	GGCATCAAATGTGACAAACGGTGTCCCTGCCACTTGAAAACTCATAGCTGTCACCCC	1140
Db	1284	 GGCATCAAATGTGACAAACGGTGTCCCTGCCACTTGAAAACTCATAGCTGTCACCCC	1343
Qy	1141	ATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGT	1200
Db	1344	 ATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGT	1403
Qy	1201	TCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGAC	1260
Db	1404	 TCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGAC	1463
Qy	1261	TGTGACAGTGTGACTGGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCT	1320
Db	1464	 TGTGACAGTGTGACTGGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCT	1523
Qy	1321	ACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAAT	1380
Db	1524	 ACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAAT	1583
Qy	1381	GATGCAGTCTGCTCTCCTGTGGACGGGTCTTGTAAGGCAAGGCTGGCACGGGGTG	1440
Db	1584	 GATGCAGTCTGCTCTCCTGTGGACGGGTCTTGTAAGGCAAGGCTGGCACGGGGTG	1643
Qy	1441	GACTGCTCCATCAGATGTCCAGTGGCACATGGGGCTTTGGCTGTAACCTAACATGCCAG	1500
Db	1644	 GACTGCTCCATCAGATGTCCAGTGGCACATGGGGCTTTGGCTGTAACCTAACATGCCAG	1703
Qy	1501	TGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGG	1560
Db	1704	 TGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGG	1763
Qy	1561	CGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAG	1620
Db	1764	 CGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAG	1823
Qy	1621	CGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTC	1680
Db	1824	 CGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTC	1883
Qy	1681	CCGGGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAAC	1740
Db	1884	 CCCGGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAAC	1943
Qy	1741	TGCTCCCTGCCCTGCTACTGTAAAAATGGGGCTTCATGCTCCCTGATGATGGCATCTGC	1800

Db	1944	TGCTCCCTGCCCTGCTACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGC	2003
Qy	1801	GAGTGTGCACCAGGCTTCCGAGGCACCACTTGTCAGAGGATCTGCTCCCCTGGTTTTTAT	1860
Db	2004	GAGTGTGCACCAGGCTTCCGAGGCACCACTTGTCAGAGGATCTGCTCCCCTGGTTTTTAT	2063
Qy	1861	GGGCATCGCTGCAGCCAGACATGCCCACAGTGCCTTCACAGCAGCGGGCCCTGCCACCAC	1920
Db	2064	GGGCATCGCTGCAGCCAGACATGCCCACAGTGCCTTCACAGCAGCGGGCCCTGCCACCAC	2123
Qy	1921	ATCACCGGCCTGTGTGACTGCTTGCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGT	1980
Db	2124	ATCACCGGCCTGTGTGACTGCTTGCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGT	2183
Qy	1981	CCCAGTGGCAGATTTGGGAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACC	2040
Db	2184	CCCAGTGGCAGATTTGGGAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACC	2243
Qy	2041	TGTAACCCCATTTGACAGATCTTGTCACTGTTACCCCGTTGGATTGGCAGTGACTGCTCT	2100
Db	2244	TGTAACCCCATTTGACAGATCTTGTCACTGTTACCCCGTTGGATTGGCAGTGACTGCTCT	2303
Qy	2101	CAACCATGTCCACCTGCCCCTGGGGCCCCAACTGCATCCACACGTGCAACTGCCATAAT	2160
Db	2304	CAACCATGTCCACCTGCCCCTGGGGCCCCAACTGCATCCACACGTGCAACTGCCATAAT	2363
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Db	2364	GGAGCTTTCTGCAGCGCCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTC	2423
Qy	2221	TACTGCACTCAGAGATGTCCTCTAGGGTTTTATGGAAAAGATTGTGCACTGATATGCCAA	2280
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Qy	2461	CCCGGATGGAAGGGAGCGAGATGTGATCAAGCTGGTGTATCATAGTTGGAAATCTGAAC	2520
Db	2664	CCCGGATGGAAGGGAGCGAGATGTGATCAAGCTGGTGTATCATAGTTGGAAATCTGAAC	2723
Qy	2521	AGCTTAAGCCGAACCACTACTGCTCTCCCTGCTGATTCTACCAGATCGGGGCCATTGCA	2580
Db	2724	AGCTTAAGCCGAACCACTACTGCTCTCCCTGCTGATTCTACCAGATCGGGGCCATTGCA	2783
Qy	2581	GGCATCATCATCTTGTCTAGTTGTTCTCTTCTACTGGCATTGTTCAATTATTTATAGA	2640
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Qy	2641	CACAAGCAGAAGGGAAAAGGAATCAAGCATGCCAGCAGTTACCTACACCCCTGCTATGAGG	2700
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Qy	2701	GTCGTCAATGCAGATTATACCATTTTCAGGAACCCTTCCTCACAGCAATGGTGGAAACGCT	2760
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Qy	2821	CACGTCAACAACAGGGACAGGATGACTGTCACGAAGTCAAAAAACAATCAACTGTTTGTG	2880
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Qy	3061	TGCTCCCTAAGCAGTTCTGAGAACCCATATGCCACTATTAAAGACCCACCTGTACTTATC	3120
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Qy	3121	CCGAAAAGCTCAGAGTGTGGTTATGTGGAGATGAAATCGCCGGGCACGAAGAGATTCCCCA	3180
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Db	3384	TATGCAGAGATCAATAACTCAACTTCAGCCAACAGGAATGTCTATGAAGTTGAACCTACA	3443
Qy	3241	GTGAGTGTGTCCAAGGAGTATTCAGCAATAATGGGCGTCTCTCCCAGGATCCATATGAC	3300
Db	3444	GTGAGTGTGTCCAAGGAGTATTCAGCAATAATGGGCGTCTCTCCCAGGATCCATATGAC	3503
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Db	3504	CTCCCAAAGAACAGTCACATCCCTTGTCATTATGACCTGCTGCCAGTCCGAGACAGTTCA	3563
Qy	3361	TCCTCCCCTAAGCAAGAGGACAGTGGAGGTAGCAGCAGCAACAGCAGCAGCAGTGA	3420
Db	3564	TCCTCCCCTAAGCAAGAGGACAGTGGAGGTAGCAGCAGCAACAGCAGCAGCAGTGA	3623
Qy	3421	TGA	3423
Db	3624	TGA	3626

RESULT 2

AB058676

LOCUS AB058676 7522 bp mRNA linear PRI 10-MAY-2001

DEFINITION Homo sapiens mRNA for MEGF10 protein (KIAA1780), complete cds.

ACCESSION AB058676

VERSION AB058676.1 GI:14017776

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)

AUTHORS Nagase,T., Nakayama,M., Nakajima,D., Kikuno,R. and Ohara,O.

TITLE Prediction of the coding sequences of unidentified human genes. XX.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro

JOURNAL DNA Res. 8 (2), 85-95 (2001)

MEDLINE 21245130

PUBMED 11347906

REFERENCE 2 (bases 1 to 7522)

AUTHORS Nakayama,M., Nagase,T., Nakajima,D., Kikuno,R. and Ohara,O.

TITLE Direct Submission

JOURNAL Submitted (27-MAR-2001) Manabu Nakayama, Kazusa DNA Rsearch
Institute, Department of Human Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:nmanabu@kazusa.or.jp,
URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3915,
Fax:81-438-52-3914)

FEATURES Location/Qualifiers

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gene

1. .7522
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ORIGIN

Query Match 100.0%; Score 3421.4; DB 9; Length 7522;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db	264	GGGACAGCATCACCTCTGAATCTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTAC	323
Qy	121	TCAGTGACTGTGCAAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGC	180
Db	324	TCAGTGACTGTGCAAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGC	383
Qy	181	ACTGACATTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCTAT	240
Db	384	ACTGACATTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCTAT	443
Qy	241	CGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTGTCCTGGATTTTATGAA	300
Db	444	CGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTGTCCTGGATTTTATGAA	503
Qy	301	AGCGGGGAAATGTGTGTCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTGCT	360
Db	504	AGCGGGGAAATGTGTGTCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTGCT	563
Qy	361	CCAAACACCTGTCAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGAT	420
Db	564	CCAAACACCTGTCAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGAT	623
Qy	421	GGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGC	480
Db	624	GGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGC	683
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Db	744	CGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATGGA	803
Qy	601	GCCACCTGCGACCACGTCACGGGGGAATGCCGCTGCCACCAGGATACACCGGAGCCTTC	660

Db	804	 GCCACCTGCGACACGTACGGGGGAATGCCGCTGCCACCAGGATACACCGGAGCCTTC	863
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Db	864	 TGTGAGGATCTTTGTCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGT	923
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Db	1164	 GCTGAGACCTGCCAGTGTGTCAACGGAGGGAAGTGTACCACGTGAGCGGCGCATGCCTC	1223
Qy	1021	TGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCTGAGGGGCTCTAC	1080
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Qy	1081	GGCATCAAATGTGACAAACGGTGTCCCTGCCACTTGGAACAACTCATAGCTGTCACCCC	1140
Db	1284	 GGCATCAAATGTGACAAACGGTGTCCCTGCCACTTGGAACAACTCATAGCTGTCACCCC	1343
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Db	1344	 ATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGT	1403
Qy	1201	TCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGAC	1260
Db	1404	 TCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGAC	1463
Qy	1261	TGTGACAGTGTGACTGGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCT	1320
Db	1464	 TGTGACAGTGTGACTGGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCT	1523
Qy	1321	ACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAAT	1380
Db	1524	 ACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAAT	1583
Qy	1381	GATGCAGTCTGCTCTCCTGTGGACGGGTCTTGACTTGCAAGGCAGGCTGGCACGGGGTG	1440
Db	1584	 GATGCAGTCTGCTCTCCTGTGGACGGGTCTTGACTTGCAAGGCAGGCTGGCACGGGGTG	1643
Qy	1441	GACTGCTCCATCAGATGTCCCAGTGGCACATGGGGCTTTGGCTGTAACCTTAACATGCCAG	1500

Db	1644	GACTGCTCCATCAGATGTCCCAGTGGCACATGGGGCTTTGGCTGTAACCTTAACATGCCAG	1703
Qy	1501	TGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGG	1560
Db	1704	TGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGG	1763
Qy	1561	CGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAG	1620
Db	1764	CGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAG	1823
Qy	1621	CGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTC	1680
Db	1824	CGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTC	1883
Qy	1681	CCGGGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAAC	1740
Db	1884	CCCGGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAAC	1943
Qy	1741	TGCTCCCTGCCCTGCTACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGC	1800
Db	1944	TGCTCCCTGCCCTGCTACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGC	2003
Qy	1801	GAGTGTGCACCAAGGCTTCCGAGGCACCACCTTGTGACAGGATCTGCTCCCCTGGTTTTAT	1860
Db	2004	GAGTGTGCACCAAGGCTTCCGAGGCACCACCTTGTGACAGGATCTGCTCCCCTGGTTTTAT	2063
Qy	1861	GGGCATCGCTGCAGCCAGACATGCCACAGTGCCTTCACAGCAGCGGGCCCTGCCACCAC	1920
Db	2064	GGGCATCGCTGCAGCCAGACATGCCACAGTGCCTTCACAGCAGCGGGCCCTGCCACCAC	2123
Qy	1921	ATCACCGGCCTGTGTGACTGCTTGCCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGT	1980
Db	2124	ATCACCGGCCTGTGTGACTGCTTGCCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGT	2183
Qy	1981	CCAGTGGCAGATTTGGGAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACC	2040
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Qy	2041	TGTAACCCCATTTGACAGATCTTGTGAGTGTACCCCGGTTGGATTGGCAGTGAAGTGTCT	2100
Db	2244	TGTAACCCCATTTGACAGATCTTGTGAGTGTACCCCGGTTGGATTGGCAGTGAAGTGTCT	2303
Qy	2101	CAACCATGTCCACCTGCCACTGGGGCCCAACTGCATCCACACGTGCAACTGCCATAAT	2160
Db	2304	CAACCATGTCCACCTGCCACTGGGGCCCAACTGCATCCACACGTGCAACTGCCATAAT	2363
Qy	2161	GGAGCTTTCTGCAGCGCCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTC	2220
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Qy	2221	TACTGCACTCAGAGATGTCTCTAGGGTTTTATGGAAAAGATTGTGCACTGATATGCCAA	2280
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Db	2664	CCCGGATGGAAGGGAGCGAGATGTGATCAAGCTGGTGTTATCATAGTTGGAAATCTGAAC	2723
Qy	2521	AGCTTAAGCCGAACCAGTACTGCTCTCCCTGCTGATTCTACCAGATCGGGGCCATTGCA	2580
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Qy	2581	GGCATCATCATTCTTGTCTAGTTGTTCTCTTCTACTGGCATTGTTCAATTATTTATAGA	2640
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RESULT 3

AK123568

LOCUS AK123568 2952 bp mRNA linear PRI 09-SEP-2003
 DEFINITION Homo sapiens cDNA FLJ41574 fis, clone CTONG2010116, weakly similar to Rattus norvegicus mRNA for MEGF6.

ACCESSION AK123568

VERSION AK123568.1 GI:34529147

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Tanigami,A., Fujiwara,T., Shibahara,T., Goto,Y., Hirao,M., Shimizu,F., Wakebe,H., Ono,T., Hishigaki,H., Watanabe,T., Ozaki,K., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2952)

AUTHORS Isogai,T. and Yamamoto,J.

TITLE Direct Submission

JOURNAL Submitted (15-JUL-2003) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and


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RAB; annotation: HRI and RAB.
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ORIGIN

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Best Local Similarity 99.9%;   Pred. No. 0;
Matches 2276;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

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Db	1258	 GGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAA	1317
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Qy 2221 TACTGCACTCAGAGATGTCCTCTAGGGTTTTATGGAAAAGATTGTGCACTGATATGCC 2278
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Db 2698 TACTGCACTCAGAGATGTCCTCTAGGGTTTTATGGAAAAGATTGTGCACTGATATGAC 2755

LOCUS BC020198 2267 bp mRNA linear PRI 16-SEP-2003
 DEFINITION Homo sapiens MEGF10 protein, mRNA (cDNA clone IMAGE:4904255), complete cds.
 ACCESSION BC020198
 VERSION BC020198.1 GI:18044365
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2267)
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 MEDLINE 22388257
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 2267)
 AUTHORS Strausberg,R.
 TITLE Direct Submission
 JOURNAL Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,

George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 40 Row: 0 Column: 4

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14192942

This clone has the following problem: The cds is short compared to the longest cds in the locus.

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ORIGIN

Query Match 49.4%; Score 1692.4; DB 9; Length 2267;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1693; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      280 ATGGTTATTTCTTTGAACTCATGCCTGAGCTTTATTTGTTTATTGTTATGCCACTGGATT 339

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Qy	241	CGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTGTCCTGGATTTTATGAA	300
Db	520	CGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTGTCCTGGATTTTATGAA	579
Qy	301	AGCGGGGAAATGTGTGTCCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTGCT	360
Db	580	AGCGGGGAAATGTGTGTCCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTGCT	639
Qy	361	CCAAACACCTGTCAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGAT	420
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Qy	421	GGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGC	480
Db	700	GGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGC	759
Qy	481	AACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGAC	540
Db	760	AACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGAC	819
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Db	820	CGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATGGA	879
Qy	601	GCCACCTGCGACCACGTACGGGGGAATGCCGCTGCCCACCAGGATACACGGAGCCTTC	660
Db	880	GCCACCTGCGACCACGTACGGGGGAATGCCGCTGCCCACCAGGATACACGGAGCCTTC	939
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Qy	721	CAAAATGGAGGAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGATG	780
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Qy	961	GCTGAGACCTGCCAGTGTGTCAACGGAGGGAAGTGTTACCACGTGAGCGGCGCATGCCTC	1020
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Qy	1021	TGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCCTGAGGGGGCTCTAC	1080
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Qy	1081	GGCATCAAATGTGACAAACGGTGTCCCTGCCACTTGGAAAACACTCATAGCTGTCACCCC	1140
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Db	1420	ATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGT	1479
Qy	1201	TCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGAC	1260
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Qy	1561	CGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAG	1620
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Qy	1621	CGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTC	1680
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RESULT 5

AR217554

LOCUS AR217554 1448 bp DNA linear PAT 25-SEP-2002

DEFINITION Sequence 9 from patent US 6416974.

ACCESSION AR217554

VERSION AR217554.1 GI:23317353

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 1448)
 AUTHORS Holtzman,D.A. and Goodearl,A.D.J.
 TITLE Tango 71 nucleic acids
 JOURNAL Patent: US 6416974-A 9 09-JUL-2002;
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ORIGIN

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Qy	1276	GGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACCCCATGCCCTCTG	1335
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Qy	1936	GACTGCTTGCC TGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGTCCCAGTGGCAGATTT	1995
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BD080296
 LOCUS BD080296 1448 bp DNA linear PAT 27-AUG-2002
 DEFINITION Tango-71, Tango-73, Tango-74, Tango-76, and Tango-83 nucleic acid molecules and polypeptides.
 ACCESSION BD080296
 VERSION BD080296.1 GI:22625899
 KEYWORDS JP 2001512681-A/5.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1448)
 AUTHORS Holtzman,D.A. and Goodearl,A.D.J.
 TITLE Tango-71, Tango-73, Tango-74, Tango-76, and Tango-83 nucleic acid molecules and polypeptides
 JOURNAL Patent: JP 2001512681-A 5 28-AUG-2001;
 MILLENNIUM PHARMACEUTICALS INC
 COMMENT OS Homo sapiens (human)
 PN JP 2001512681-A/5
 PD 28-AUG-2001
 PF 06-AUG-1998 JP 2000506335
 PR 06-AUG-1997 US 60/054966,05-SEP-1997 US 60/058108 PI
 DOUGLAS A HOLTZMAN,ANDREW D J GOODEARL
 PC C12N15/09,C07K14/47,C07K16/18,C12N5/10,C12P21/02,C12Q1/68, PC
 G01N33/15,
 PC G01N33/50,G01N33/53//C12P21/08,C12N15/00,C12N5/00 CC
 Tango-71, Tango-73, Tango-74, Tango-76, and Tango-83 nucleic acid
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 FH Key Location/Qualifiers
 FT source 1. .1448
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ORIGIN

Query Match 41.7%; Score 1425.8; DB 6; Length 1448;
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Qy 1216 GGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTGTGACT 1275
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Db 318 GCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGGCGCGGGGAGAAATGC 377

Qy 1576 GAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAGCGCTGCGACTGCAGC 1635
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Db 378 GAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAGCGCTGCGACTGCAGC 437

Qy 1636 CACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTCCCGGGATGGTCAGGT 1695
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Db 798 GGGAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACCTGTAACCCCATTGAC 857

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Db 858 AGATCTTGTGAGTGTACCCCGGTTGGATTGGCAGTGACTGCTCTCAACCATGTCCACCT 917

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Qy 2176 GCCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTCTACTGCACTCAGAGA 2235
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Db 978 GCCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTCTACTGCACTCAGAGA 1037

Qy 2236 TGTCTCTAGGGTTTTATGGAAAAGATTGTGCACTGATATGCCAATGTCAAACGGAGCT 2295
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Qy      2296 GACTGCGACCACATTTCTGGGCAGTGTACTTGCCGCACTGGATTTCATGGGACGGCACTGT 2355
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Db      1098 GACTGCGACCACATTTCTGGGCAGTGTACTTGCCGCACTGGATTTCATGGGACGGCACTGT 1157

Qy      2356 GAGCAGAAGTGCCCTTCAGGAACATATGGCTATGGCTGTCGCCAGATATGTGATTGTCTG 2415
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Db      1158 GAGCAGAAGTGCCCTTCAGGAACATATGGCTATGGCTGTCGCCAGATATGTGATTGTCTG 1217

Qy      2416 AACAACTCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGCCCCGGATGGAAGGGA 2475
          |||
Db      1218 AACAACTCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGCCCCGGATGGAAGGGA 1277

Qy      2476 GCGAGATGTGATCAAGCTGGTGTTCATAGTTGGAAATCTGAACAGCTTAAGCCGAACC 2535
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Qy      2536 AGTACTGCTCTCCCTGCTGATTCCCTACCAGATCGGGGCCATTGCAGGCATCATCATTCTT 2595
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Db      1338 AGTACTGCTCTCCCTGCTGATTCCCTACCAATCGGGGCCATTGCAGGCATCATCATTCTT 1397

Qy      2596 GTCCTAGTTGTTCTCTTCCTACTGGCATTGTTTCATTATTTATAGACACA 2644
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Db      1398 GTCCTAGTTGTTCTCTTCCTACTGGCATTGTTTCATTATTTATAGACACA 1446

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RESULT 7

AB058677

LOCUS AB058677 5702 bp mRNA linear PRI 10-MAY-2001

DEFINITION Homo sapiens mRNA for MEGF11 protein (KIAA1781), complete cds.

ACCESSION AB058677

VERSION AB058677.1 GI:14017778

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)

AUTHORS Nagase,T., Nakayama,M., Nakajima,D., Kikuno,R. and Ohara,O.

TITLE Prediction of the coding sequences of unidentified human genes. XX.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro

JOURNAL DNA Res. 8 (2), 85-95 (2001)

MEDLINE 21245130

PUBMED 11347906

REFERENCE 2 (bases 1 to 5702)

AUTHORS Nakayama,M., Nagase,T., Nakajima,D., Kikuno,R. and Ohara,O.

TITLE Direct Submission

JOURNAL Submitted (27-MAR-2001) Manabu Nakayama, Kazusa DNA Research
Institute, Department of Human Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:nmanabu@kazusa.or.jp,
URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3915,
Fax:81-438-52-3914)

FEATURES Location/Qualifiers

source 1..5702

/organism="Homo sapiens"

/mol_type="mRNA"

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/note="vector:pBluescript II SK plus"
gene 1. .5702
/ gene="MEGF11"
CDS 160. .3069
/ gene="MEGF11"
/ note="KIAA1781 protein
Start codon is not confirmed. fg06971 cDNA clone for
KIAA1781 has a 119bp insertion after the position 2642 of
the sequence of KIAA1781
gene encoding protein with multiple EGF-like-domains"
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ORIGIN

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Query Match          35.1%;  Score 1200.6;  DB 9;  Length 5702;
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Matches 1670;  Conservative 0;  Mismatches 739;  Indels 6;  Gaps 2;

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Db      234 CGCCCTGTGTACGGAGGAGTGTGTGCACGGCCGCTGCGTTTCCCCGGACACCTGCCACTG 293

Qy      378 TGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCCTGCGATGGTGATCACTGGGGTCC 437
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Qy      438 CCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGCAACCCCATCACCGGGGC 497
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Db      354 CCACTGCAGCAACCGGTGCCAGTGCCAGAACGGCGCCCTGTGTAACCCCATCACAGGCGC 413

Qy      498 TTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGACCGCTGTGAGCAGGGCAC 557
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Db      414 CTGCGTGTGCGCCGCCGGCTTCCGTGGATGGCGCTGCGAGGAGCTCTGCGCGCCTGGCAC 473

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Qy	558	CTATGGTAAACGACTGTGCATCAGAGATGCCAGTGCCAGAATGGAGCCACCTGCCACCACGT	617
Db	474	CCACGGCAAGGGATGCCAGCTGCCGTGCCAGTGCCGACACGGTGCCAGCTGCGACCCCCG	533
Qy	618	CACGGGGGAATGCCGCTGCCCACCAGGATACACCGAGCCTTCTGTGAGGATCTTTGTCC	677
Db	534	CGCCGGCGAGTGCCTCTGCGCACCTGGCTACACCGGCGTCTACTGCGAGGAGCTGTGCC	593
Qy	678	TCCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGTCAAATGGAGGAGTGTG	737
Db	594	TCCTGGGAGCCATGGAGCTCACTGTGAGCTGCGCTGCCCCTGTGAGAATGGGGGCACCTG	653
Qy	738	TCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGATGGGCACAGTGTGTGGTCA	797
Db	654	CCACCACATCACTGGCGAGTGTGCCTGCCCCCAGGCTGGACGGGAGCAGTGTGTGCCA	713
Qy	798	GCCTTGCCCCGAGGGTGCCTTTGGAAAGAACTGTTCCCAAGAATGCCAGTGCCATAATGG	857
Db	714	GCCCTGCCACCACGAGGACATTGGCCAGAACTGCAGCCAGGATTGTCTTGCCACCATGG	773
Qy	858	AGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCAGGATACACAGGGGAACG	917
Db	774	AGGGCAGTGTGACCACGTGACTGGACAGTGCCACTGTACAGCTGGATACATGGGGGACAG	833
Qy	918	GTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGTGCTGAGACCTGCCAGTG	977
Db	834	GTGCCAAGAGGAGTGGCCCTTCGGGTCTTCGGCTTCCAGTGCTCACAGCGCTGTGACTG	893
Qy	978	TGTCAACGGAGGGAAGTGTACCACGTGAGCGGCGCATGCCTCTGTGAAGCAGGCTTTGC	1037
Db	894	CCACAATGGGGGGCAGTGTTCACCCACCACGGGTGCCTGCGAGTGTGAGCCTGGCTACAA	953
Qy	1038	TGGCGAGCGCTGCGAAGCACGCCTGTGTCTGAGGGGCTCTACGGCATCAAATGTGACAA	1097
Db	954	GGGCCCACGCTGCCAGGAGCGACTGTGCCCGAGGGGCTGCATGGCCCAGGCTGCACCCCT	1013
Qy	1098	ACGGTGTCCCTGCCACTTGAAAACTCATAGCTGTCACCCCATGTCTGGAGAGTGTGC	1157
Db	1014	GCCCTGCCCTGTGACGCTGACAAACACCATCAGCTGCCACCCAGTAAGTGGAGCTGTGAC	1073
Qy	1158	CTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGTTCTCCTGGATTCTACGG	1217
Db	1074	CTGCCAGCCAGGCTGGTCTGGTCACCACTGCAATGAATCCTGCCCTGTTGGCTACTATGG	1133
Qy	1218	GGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTGTGACTGG	1277
Db	1134	CGATGGCTGCCAGCTGCCTTGACCTGTCAGAATGGCGCCGACTGCCACAGCATCACTGG	1193
Qy	1278	AAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACCCCATGCCCTCTGGG	1337
Db	1194	GGGCTGCACTTGTGCTCCGGGCTTCATGGGAGAGGTCTGTGCCGTTTCCTGTGCAGCAGG	1253
Qy	1338	AACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAATGATGCAGTCTGCTCTCC	1397
Db	1254	GACCTATGGCCCCAACTGCTCGTCCATCTGTAGCTGTAACAATGGTGGCACCTGCTCCCC	1313
Qy	1398	TGTGGACGGGTCTTGTAAGGCAAGGCAGGCTGGCACGGGGTGGACTGCTCCATCAGATG	1457

Db	1314	AGTAGATGGCTCCTGTACCTGCAAGGAAGGGTGGCAGGGCCTGGACTGCACCCTGCCATG	1373
Qy	1458	TCCCAGTGGCACATGGGGCTTTGGCTGTAACCTAACATGCCAGTGCCTCAACGGGGGAGC	1517
Db	1374	TCCCAGTGGGACGTGGGGCCTGAACTGCAACGAGAGCTGCACCTGTGCCAATGGGGCAGC	1433
Qy	1518	CTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGGCGCGGGGAGAAATGCGA	1577
Db	1434	CTGCAGCCCATAGACGGCTCCTGCTCCTGCACTCCTGGCTGGCTGGGAGACACCTGTGA	1493
Qy	1578	ACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAGCGCTGCCACTGCAGCCA	1637
Db	1494	GCTGCCTTGCCCGGATGGCACATTTGGGCTGAACTGCAGTGAACACTGTGACTGCAGCCA	1553
Qy	1638	CGCAGATGGCTGCCACCCTACCACGGGGCCATTGCCGCTGCCTCCCGGGATGGTCAGGTGT	1697
Db	1554	TGCTGATGGATGTGACCCCGTCACAGGCCACTGCTGCTGCCTGGCCGGATGGACAGGCAT	1613
Qy	1698	CCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAACTGCTCCCTGCCCTGCTA	1757
Db	1614	CCGCTGTGACAGCACGTGTCCACCTGGCCGCTGGGGCCCCAACTGCTCTGTCTCCTGCAG	1673
Qy	1758	CTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGCGAGTGTGCACCAGGCTT	1817
Db	1674	CTGTGAGAAATGGAGGCTCCTGCTCCCCAGAGGATGGGAGCTGCGAGTGTGCCCTTGCTT	1733
Qy	1818	CCGAGGCACCACTTGTCAGAGGATCTGCTCCCCTGGTTTTTATGGGCATCGCTGCAGCCA	1877
Db	1734	CCGAGGACCCTTATGCCAGAGAATCTGCCCCCTGGGTTCATGGCCACGGCTGCGCCCA	1793
Qy	1878	GACATGCCCACAGTGC GTTCACAGCAGCGGGCCCTGCCACCACATCACCGGCCTGTGTGA	1937
Db	1794	GCCATGCCCCCTCTGCGTGACAGCAGCAGGCCCTGCCACCACATCAGCGGCATCTGTGA	1853
Qy	1938	CTGCTTGCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGTCCCAGTGGCAGATTTGG	1997
Db	1854	GTGCCTCCCAGGATTCTCTGGAGCTCTCTGCAACCAAGTGTGTGCTGGAGGATACTTTGG	1913
Qy	1998	GAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACCTGTAACCCCATTGACAG	2057
Db	1914	GCAGGACTGTGCCAGCTCTGCTCCTGTGCCAACAAACGGGACCTGCAGCCCTATCGATGG	1973
Qy	2058	ATCTTGTCAGTGTTACCCCGGTTGGATTGGCAGTGA CTGCTCTCAACCATGTCCACCTGC	2117
Db	1974	CTCCTGCCAGTGCTTTCTGGATGGATTGGCAAGGACTGCTCACAGGCTTGCCACCCCGG	2033
Qy	2118	CCACTGGGGCCCCAACTGCATCCACACGTGCAACTGCCATAATGGAGCTTTCTGCAGCGC	2177
Db	2034	GTTCTGGGGCCCCGCCTGCTTCCACGCATGCAGCTGCCACAACGGGGCGAGCTGCAGCGC	2093
Qy	2178	CTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTCTACTGCACTCAGAGATG	2237
Db	2094	CGAGGACGGGGCTGCCACTGCACCCCTGGCTGGACTGGACTCTCTGCACACAGCGCTG	2153
Qy	2238	TCCTCTAGGGTTTTATGGAAAAGATTGTGCACTGATATGCCAATGTCAAAACGGAGCTGA	2297

Db 2154 CCCAGCAGCATT TTTTGGGAAGGACTGTGGGCGCGTATGCCAGTGT CAGAATGGCGCCAG 2213

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Db 2214 CTGTGACCACATCAGTGGCAAGTGCACCTGCCGCACAGGCTTACC GGGCAACACTGTGA 2273

Qy 2358 GCAGAAGTGCCCTTCAGGAACATATGGCTATGGCTGT CGCCAGATATGTGATTGTCTGAA 2417
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Db 2274 GCAGAGATGTGCCCCAGGAACCTTTGGCTATGGGTGTCAGCAGCTATGTGAGTGCATGAA 2333

Qy 2418 CAACTCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGCCCCGGATGGAAGGGAGC 2477
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Db 2334 CAACTCCACCTGTGACCATGTCACCGGCACCTGTTACTGCAGCCCTGGCTTCAAAGGAAT 2393

Qy 2478 GAGATGTGATCAAGCTGGTGT TATCATAGTTGAAATCTGAACAGCTTAAGCCGAACCAG 2537
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Db 2394 CAGGTGTGACCAAGCTGCCCTCATGATGGAGG---AGCTGAATCCCTACACCAAGATCAG 2450

Qy 2538 TACTGCTCTCCCTGCTGATTCCTACCAGATCGGGGCCATTGCAGGCATCATCATTCTTGT 2597
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Db 2451 CCCAGCACTGGGTGCAGAGCGGCACCTCGGTGGGTGCTGT CACAGGCATCATGCTCCTGTT 2510

Qy 2598 CCTAGTTGTTCTCTTCTACTGGCATTGTT CATTATTTATAGACACAAGCAGAAGGGAAA 2657
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Db 2511 ATTCTTCATTGTGGTGCTGCTGGGCCTATTTGCCTGGCATCGGCGGCGGCAGAAAGAGAA 2570

Qy 2658 GGAATCAAGCATG---CCAGCAGTTACCTACACCCCTGCTATGAGGGTCGTCAATGCAGA 2714
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Db 2571 GGGCCGAGACCTGGCTCCCCGTGTCTCCTACACACCTGCCATGAGGATGACCAGCACC GA 2630

Qy 2715 TTATACCATTTCAGG 2729
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Db 2631 CTA CTCTCCCTCTCAGG 2645

RESULT 8

AK122555

LOCUS AK122555 5278 bp mRNA linear ROD 15-MAR-2003

DEFINITION Mus musculus mRNA for mKIAA1781 protein.

ACCESSION AK122555

VERSION AK122555.1 GI:28972841

KEYWORDS FLI_CDNA.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Okazaki,N., Kikuno,R., Ohara,R., Inamoto,S., Aizawa,H., Yuasa,S., Nakajima,D., Nagase,T., Ohara,O. and Koga,H.

TITLE Prediction of the coding sequences of mouse homologues of KIAA gene: II. The complete nucleotide sequences of 400 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries

JOURNAL DNA Res. 10, 35-48 (2003)

REFERENCE 2 (bases 1 to 5278)

AUTHORS Okazaki,N., Kikuno,R., Nagase,T., Ohara,O. and Koga,H.

TITLE Direct Submission

[illegible]

Qy	1633	AGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCCTCCCGGGATGGTCA	1692
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Qy	1693	GGTGTCCTACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAACTGCTCCCTGCCC	1752
Db	1021	GGCATCCGCTGTGATAGCACGTGTCTCCAGGTGCGTGCGGGCCCCAACTGTTCACTGTCC	1080
Qy	1753	TGCTACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGCGAGTGTGCACCA	1812
Db	1081	TGCAGCTGTGAGAACGGAGGTTCTGCTCCCCGGAGGACGGGAGCTGCGAGTGTGCCCT	1140
Qy	1813	GGCTTCCGAGGCACTTGTCTCAGAGGATCTGCTCCCCTGGTTTTTATGGGCATCGCTGC	1872
Db	1141	GGCTTTCGAGGACCCTTATGTCTCAGAGAATCTGCCCACCAGGATTCACGGCCATGGCTGC	1200
Qy	1873	AGCCAGACATGCCACAGTGCCTTCACAGCAGCGGGCCCTGCCACCACATCACCGGCCTG	1932
Db	1201	GCCCAGCCTTGTCCCCTCTGCGTGCACAGCGGGGGCCCTGCCACCACATCAGTGGTATC	1260
Qy	1933	TGTGACTGCTTGCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGTCCAGTGGCAGA	1992
Db	1261	TGTGAGTGCCTGCCAGGATTCTCTGGAGCCTTGTGCAACCAAGTGTGTGCTGGAGGGCAC	1320
Qy	1993	TTTGGGAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACCTGTAACCCCATT	2052
Db	1321	TTCGGGCAGGACTGTGCCAGCTCTGTTCTGTGCCAACAAATGGGACCTGCAGCCCCATC	1380
Qy	2053	GACAGATCTTGTCTAGTGTACCCCGTTGGATTGGCAGTGAAGTGTCTCAACCATGTCCA	2112
Db	1381	GATGGCTCCTGTCTAGTGTCTCCCTGGGTGGATTGGCAAGGACTGCTCACAGGCCTGCCCA	1440
Qy	2113	CCTGCCCACTGGGGCCCCAACTGCATCCACACGTGCAACTGCCATAATGGAGCTTTCTGC	2172
Db	1441	TCTGGGTTCTGGGGCTCTGCCTGCTCCACACATGCAGCTGCCACAACGGGGCGAGCTGC	1500
Qy	2173	AGCGCCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTCTACTGCACTCAG	2232
Db	1501	AGCGCCGAGGATGGGGCCTGCCACTGCACCCCTGGCTGGACTGGACTCTCTGCACGCAG	1560
Qy	2233	AGATGTCCTCTAGGGTTTTATGGAAAAGATTGTGCACTGATATGCCAATGTCAAAACGGA	2292
Db	1561	CGTTGCCCTTCAGCATTTTTTGGGAAGGACTGTGGGCACATATGCCAGTGTCTCAGAATGGA	1620
Qy	2293	GCTGACTGCGACCACATTTCTGGGCAGTGTACTTGCCGCACTGGATTTCATGGGACGGCAC	2352
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Qy	2353	TGTGAGCAGAAGTGCCCTTCAGGAACATATGGCTATGGCTGTCTGCCAGATATGTGATTGT	2412
Db	1681	TGTGAACAGAGATGTGCCCTGGAACCTTTGGATATGGGTGTCTCAGCAGCTATGTGAGTGC	1740
Qy	2413	CTGAACAACTCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGCCCCGGATGGAAG	2472
Db	1741	ATGAACAATGCCACTTGTGACCACGTCACCTGGTACCTGTTACTGTAGCCCGGATTCAAA	1800

Qy	2473	GGAGCGAGATGTGATCAAGCTGGTGTATCATAGTTGGAATCTGAACAGCTTAAGCCGA	2532	
Db	1801			
		1801 GGAATCAGGTGTGACCAAGCTGCCCTCATGATGGATG---AGCTGAATCCCTACACCAAG	1857	
Qy	2533	ACCAGTACTGCTCTCCCTGCTGATTCCTACCAGATCGGGGCCATTGCAGGCATCATCATT	2592	
Db	1858			
		1858 ATCAGTCCAGCTCTGGGAGCAGAGCGGCACTCAGTGGGTGCTGTCCACGGCATCGTTCTC	1917	
Qy	2593	CTTGTCCTAGTTGTTTCTCTTCCTACTGGCATTGTTTCATTATTTATAGACACAAGCAGAAG	2652	
Db	1918			
		1918 CTGTTGTTCTCTGGTGGTGGTGTCTGTGGGCCTGTTTGCCTGGCGACGGAGGCGGCAGAAA	1977	
Qy	2653	GGAAAGGAATCAAGCATG---CCAGCAGTTACCTACACCCCTGCTATGAGGGTCGTCAAT	2709	
Db	1978			
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Qy	2710	GCAGATTATACCATTTTCAGGAACCCCTTCCTCACAGCAATGGTGGAAAC-----GCTAAT	2763	
Db	2038			
		2038 ACAGACTACTCTCTCTCAGATTTGTCTCAAAGTAGCAGCCATGCCCAGTGCTTTTCCAAT	2097	
Qy	2764	AGCCACTACTTCACCAATCCCAGTTACCACACGCTCACCCAGTGTGCCACATCCCCTCAC	2823	
Db	2098			
		2098 GCCAGCTACCACACACTGGCGTGTGGGGGGCTGCCACCAGCCAGGCCAGCACTCTGGAC	2157	
Qy	2824	GTCAACAACAGGGACAGGATGACTGTCACG-AAGTCAAAAAACAATCAACTGTTTGTGAA	2882	
Db	2158			
		2158 AGGAACAGCCCCACCAAGCTCAGTAACAAGTCCCTTGACAGAGACACAGCAGGCTGGACC	2217	
Qy	2883	TCTTAAAAATGTGAACCCTGGGAAGA-----GAGGCCCTGTGGGGGACTG	2927	
Db	2218			
		2218 CCCTACAGCTATGTGAACGTGTTAGACTCCCATTTCAGATCAGTGCCCTGGAGGCCAGG	2277	
Qy	2928	CACTGGGACATTGCCGGCTGACTGGAAACATGGCGGCT-----ACCTCAAC	2973	
Db	2278			
		2278 TACCCGCCCAGGACTTCTACATTGAACTTAGACACCTCAGCCGCCATGCTGAGCCACAC	2337	
Qy	2974	GAGCTCGGTGCTTTTGGACTTGACAGAAG-----CTATATGGGAAAATCCTTA	3021	
Db	2338			
		2338 TCACCAGGCACTTGTGGAATGGACAGACGT'CAGAACACATACATTATGGACAAAGGCTTC	2397	
Qy	3022	AAAGACCTGGGAAAGAATTCTGAATATAATTCAAGTAAGTCTCCCTAAGCAGTTCTGAG	3081	
Db	2398			
		2398 AAAGATTACATGAAAGAATCTGTGTGCAGTTCTAGCACTTGCTCCTTGAACAGCAGTGAA	2457	
Qy	3082	AACCCATATGCCACTATTAAAGACCCACCTGTACTTATCCCGAAAAGCTCAGAGTGTGGT	3141	
Db	2458			
		2458 AACCTTACGCCACAATTAAGGACCCACCATCCTCACCTGCAAGCTTCCAGAAAGCAGT	2517	
Qy	3142	TATGTGGAGATGAAATCGCCGGCACGAAGAGATTCCCCATATGCAGAGATCAATAACTCA	3201	
Db	2518			
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Qy	3202	ACTTCAGCCAACAGGAATGTCTATGAAGTTGAACCTACAGTGAGTGTGTCCAAGGAGTA	3261	
Db	2578			
		2578 TCGACATCTAATAAAAAATATATATGAAGTTGAGCCACAGTCAGTGTGGTCCAAGAAGGC	2637	
Qy	3262	TTCAGCAATAATGGGCGTCTCTCCAGGATCCATATGACCTCCCAAAGAACAGTCACATC	3321	

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Db      2638 CGAGGTCATAACTCCAGCTATATCCAGAATCCATACGACCTACCTAAGAACAGCCATATT 2697

QY      3322 CCTTGTCATTATGACCTGCTGCCAGTCCGAGACAGTTCATCC 3363
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Db      2698 CCTGGTCACTATGACCTCCTCCCAGTAAGACAGAGCCCTGCC 2739

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RESULT 9

HSM805375

LOCUS HSM805375 3281 bp mRNA linear PRI 12-JUL-2002

DEFINITION Homo sapiens mRNA; cDNA DKFZp434L121 (from clone DKFZp434L121).

ACCESSION AL834326

VERSION AL834326.1 GI:21739945

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3281)

AUTHORS Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.

TITLE Direct Submission

JOURNAL Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY

COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp434L121) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at <http://mips.gsf.de/proj/cDNA/>.

FEATURES

source

Location/Qualifiers

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DH10B; sites NotI + SalI"

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CDS

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ORIGIN

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Best Local Similarity 69.2%; Pred. No. 8.4e-218;
Matches 1012; Conservative 0; Mismatches 450; Indels 0; Gaps 0;

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Qy	1081	GGCATCAAATGTGACAAACGGTGTCCCTGCCACTTGGAAAACACTCATAGCTGTCAACCCC	1140
Db	318	GGCCCAGGCTGCACCCTGCCCTGCCCTGTGACGCTGACAACACCATCAGCTGCCACCCA	377
Qy	1141	ATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGT	1200
Db	378	GTAAGTGGAGCTTGTACCTGCCAGCCAGGCTGGTCTGGTCACCACTGCAATGAATCCTGC	437
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Qy	1261	TGTGACAGTGTGACTGGAAAGTGACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCT	1320
Db	498	TGCCACAGCATCACTGGGGGCTGCACTTGTGCTCCGGGCTTCATGGGAGAGGTCTGTGCC	557
Qy	1321	ACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCCCTCTCGCTGTGGCTGTAAAAAT	1380
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Db	678	GACTGCACCCTGCCATGTCCCAGTGGGACGTGGGG	737
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Db	738	TGTGCCAATGGGGCAGCCTGCAGCCCCATAGACGG	797
Qy	1561	CGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGG	1620
Db	798	CTGGGAGACACCTGTGAGCTGCCTTGCCCGGATGG	857
Qy	1621	CGCTGCGACTGCAGCCACGCAGATGGCTGCCACC	1680
Db	858	CACTGTGACTGCAGCCATGCTGATGGATGTGACCC	917
Qy	1681	CCGGGATGGTCAGGTGTCCACTGTGACAGCGTGT	1740
Db	918	GCCGGATGGACAGGCATCCGCTGTGACAGCACGT	977
Qy	1741	TGCTCCCTGCCCTGCTACTGTAAAAATGGGGCTTC	1800
Db	978	TGCTCTGTCTCCTGCAGCTGTGAGAATGGAGGCT	1037
Qy	1801	GAGTGTGCACCAGGCTTCCGAGGCACCACTGTGTC	1860
Db	1038	GAGTGTGCCCTTGGCTTCCGAGGACCCTTATGCC	1097
Qy	1861	GGGCATCGCTGCAGCCAGACATGCCACAGTGC GTT	1920
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Qy	1921	ATCACCGGCCTGTGTGACTGCTTGCCTGGCTTTC	1980
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RESULT 10

AF444274

LOCUS AF444274 4290 bp mRNA linear ROD 06-DEC-2001

DEFINITION Mus musculus Jedi protein mRNA, complete cds.

ACCESSION AF444274

VERSION AF444274.1 GI:17386052

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 4290)

AUTHORS Krivtsov,A.V., Zinovyeva,M.V., Hendrikx,J., Visser,J.W.M. and
Belyavsky,A.V.

TITLE Jedi is a novel DSL and EGF-like repeat motif-containing protein
expressed on non-differentiated hematopoietic cells

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 4290)

AUTHORS Krivtsov,A.V., Zinovyeva,M.V., Visser,J.W.M. and Belyavsky,A.V.

TITLE Direct Submission

JOURNAL Submitted (07-NOV-2001) Stem Cell Biology, Lindsley F. Kimball
Research Institute, New York Blood Center, 310 East 67 Street, New
York, NY 10021, USA

FEATURES Location/Qualifiers

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Qy	731	GAGTGTGTTCATCACGTCACCTGGAGAATGCTCTTGCCCTTCTGGCTGGATGGGCACAGTGT	790
Db	847	GTGTTCTCCTCAGGGCTCCCAAGGCTCCTGCAGCTGCCACCGGGCTGGATGGGTGTCATTT	906
Qy	791	GTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAATGCCAGTGCC	850
Db	907	GTTCCCTGCCATGCCCAGAGGGTTTCATGGACCAACTGTACTCAGGAATGTCGCTGCC	966
Qy	851	ATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCAGGATACACAG	910
Db	967	ACAACGGTGGCCTCTGTGACAGGTTTACTGGGCAGTGCCACTGTGCTCCTGGCTATATCG	1026
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Qy	971	GCCAGTGTGTCAACGGAGGGAAGTGTACCACGTGAGCGGCGCATGCCTCTGTGAAGCAG	1030
Db	1087	GTGACTGTGCTCCTGGCGCCCGTTGCTTTCCTGCTAATGGCGCGTGTCTGTGCGAACATG	1146
Qy	1031	GCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCTGAGGGGCTCTACGGCATCAAAT	1090
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Qy	1091	GTGACAAACGGTGTCCCTGCCACTTGGAACAACTCATAGCTGTACCCCATGTCTGGAG	1150
Db	1207	GCCAGGAGCCCTGCACCTGCGACCCAGAACACAGTCTCAGCTGCCACCCGATGCACGGCG	1266
Qy	1151	AGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGTTCTCCTGGAT	1210
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Qy	1211	TCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAATGGGGCAGACTGTGACAGTG	1270
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Qy	1391	GCTCTCCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCACGGGGTGGACTGCTCCA	1450
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Qy	1451	TCAGATGTCCCAGTGGCACATGGGGCTTTGGCTGTAACCTAACATGCCAGTGCCTCAACG	1510
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Db	1687	ACTGCCAGCTTCCCTGCCCCAAGGGACAGTTTGGTGAAGGCTGTGCCAGTGTCTGTGACT	1746
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Db	2041	CCTGCTCCTGCCTGGCGGGCTGGACAGGCCCTGACTGCTCTGAGGCATGTCCCCCAGGCC	2100
Qy	1991	GATTTGGGAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACCTGTAACCCCA	2050
Db	2101	ACTGGGGACTCAAATGCTCCCAACTCTGCCAGTGTGTCATCATGGTGGGACCTGCCACCCCC	2160
Qy	2051	TTGACAGATCTTGTGAGTGTACCCCGGTTGGATTGGCAGTGAAGTGTCTCAACCATGTC	2110
Db	2161	AGGATGGGAGCTGTATCTGCACGCCAGGCTGGACTGGACCCAACCTGCTTGAAGGCTGCC	2220
Qy	2111	CACCTGCCCACTGGGGCCCAAACCTGCATCCACACGTGCAACTGCCATAATGGAGCTTTCT	2170
Db	2221	CACCAAGAATGTTTGGTGTCAACTGCTCCCAGCTATGTGAGTGTGATCTCGGAGAGATGT	2280
Qy	2171	GCAGCGCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTCTACTGCACTC	2230
Db	2281	GCCACCCACAGACTGGGGCTTGTGTCTGTCCCCCAGGACACAGTGGTGCAGACTGCAAAA	2340
Qy	2231	AGAGATGTC	2239
Db	2341	TGGGAAGCC	2349

RESULT 11

AF461685

LOCUS AF461685 4539 bp mRNA linear ROD 21-JAN-2002

DEFINITION Mus musculus Jedi-736 protein mRNA, complete cds.

ACCESSION AF461685

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VERSION      AF461685.1  GI:18252657
KEYWORDS     .
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1 (bases 1 to 4539)
AUTHORS      Krivtsov,A.V., Zinovyeva,M.V., Hendrikx,J., Visser,J.W.M. and
              Belyavsky,A.V.
TITLE        Jedi is a novel DSL and EGF-like repeat motif-containing protein
              expressed on non-differentiated hematopoietic cells
JOURNAL       Unpublished
REFERENCE    2 (bases 1 to 4539)
AUTHORS      Krivtsov,A.V., Zinovyeva,M.V., Visser,J.W.M. and Belyavsky,A.V.
TITLE        Direct Submission
JOURNAL       Submitted (20-DEC-2001) Stem Cell Biology, Lindsley F. Kimball
              Research Institute, New York Blood Center, 310 East 67th Street,
              New York, NY 10021, USA
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ORIGIN
Query Match      18.9%;   Score 648.6;   DB 10;   Length 4539;
Best Local Similarity  57.3%;   Pred. No. 8.9e-189;
Matches 1236;   Conservative    0;   Mismatches 909;   Indels    12;   Gaps    3;

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Qy     134 AAGAGTCATACCCACATCCCTTTGATCAAAT---TTACTACACGAGCTGCACTGACATTC 190

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Db	243	AGGACCCCCACACCTGTGCCCAGCCTACGGTTGTCTACCGGACTGTGTACCGTCAGGTGG	302
Qy	251	AGAAGACTATGTATAGGCGCAAGTCTCAGTGTTGTCTCGGATTTTATGAAAGCGGGGAAA	310
Db	303	TGAAGATGGACTCCCCGCCACGCCTGCAGTGCTGTAGGGGTACTACGAGAGCAGAGGGG	362
Qy	311	TGTGTGTCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTGCTCCAAACACCT	370
Db	363	CCTGTGTCCCACTCTGTGCCCAGGAGTGTGTCCATGGTCGCTGTGTGGCTCCGAATCAGT	422
Qy	371	GTCAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGATGGTGATCACT	430
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Qy	431	GGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAATGGGGCTCTGTGCAACCCCATCA	490
Db	483	GGGGACCACAGTGTGACAAGTTCTGCCACTGTGGCAACAACAGTTCCTGTGATCCCAAGA	542
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Qy	731	GAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGATGGGCACAGTGT	790
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Qy	791	GTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAATGCCAGTGCC	850
Db	840	GTTCCCTGCCATGCCAGAGGGTTTCCATGGACCCAAGTGTACTCAGGAATGTCGCTGCC	899
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Qy	911	GGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGTGCTGAGACCT	970
Db	960	GGGATCGGTGCCAAGAAGAGTGCCCCGTGGGCCGCTTTGGTCAAGACTGTGCTGAGACCT	1019
Qy	971	GCCAGTGTGTCAACGGAGGGAAGTGTTACCACGTGAGCGGCGCATGCCTCTGTGAAGCAG	1030

Db 1020 GTGACTGTGCTCCTGGCGCCCGTTGCTTTCCTGCTAATGGCGCGTGTCTGTGCGAACATG 1079
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 Db 1320 ACAGCGGCCTCTGTGCGGTGCGCGCCAGGATACAGGGACCTCACTGCGCTAACCTATGTC 1379
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 Db 1380 CACCGGACACTTATGGGATCAACTGTTTCCTCCGCTGCTCCTGTGAAAAATGCCATTGCCT 1439
 Qy 1391 GCTCTCCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCACGGGGTGGACTGCTCCA 1450
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 Db 1500 TTCCCTGTCCCTTGGCACCTGGGGCTTCAATTGCAATGCCAGTTGCCAGTGTGCCACAG 1559
 Qy 1511 GGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGGCGCGGGGAGA 1570
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 Qy 1571 AATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAAC TGCTGAGCGCTGCGACT 1630
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 Db 2214 GCCACCCACAGACTGGGGCTTGTGTCTGTCCCCCAGGACACAGTGGTGCAGACTGCA 2270

RESULT 12

AF440279

LOCUS AF440279 4482 bp mRNA linear ROD 20-NOV-2001

DEFINITION Mus musculus MEGF12 (Megf12) mRNA, complete cds.

ACCESSION AF440279

VERSION AF440279.1 GI:17017250

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 4482)

AUTHORS Ivanova,N.B. and Lemischka,I.R.

TITLE The global gene expression profiling of the hematopoietic stem cell

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 4482)

AUTHORS Ivanova,N.B. and Lemischka,I.R.

TITLE Direct Submission

JOURNAL Submitted (25-OCT-2001) Molecular Biology, Princeton University, Washington Road, Princeton, NJ 08544, USA

FEATURES Location/Qualifiers

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Query Match 18.9%; Score 646.2; DB 10; Length 4482;
Best Local Similarity 57.1%; Pred. No. 5e-188;
Matches 1239; Conservative 0; Mismatches 918; Indels 12; Gaps 3;

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Qy	191	TAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCTATCGACATGGGG	250
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Qy	251	AGAAGACTATGTATAGGCGCAAGTCTCAGTGTGTCTCGGATTTTATGAAAGCGGGGAAA	310
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Qy	371	GTCAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGATGGTGATCACT	430
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Qy	491	CCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGACCGCTGTGAGC	550
Db	810	GTGGGACGTGCTTTTGCCCTCTGGCCTGCAGCCCCCAACTGCCTTCAGCCCTGCCCTG	869
Qy	551	AGGGCACCTATGGTAACGACTGTTCATCAGAGATGCCAGTGCCAGAATGGAGCCACCTGCG	610
Db	870	CCGGCCACTATGGTCCTGCCTGCCAGTTTGATTGCCAGTGC---TATGGGGCATCCTGTG	926
Qy	611	ACCACGTACAGGGGGAATGCCGCTGCCACCAGGATACACCGGAGCCTTCTGTGAGGATC	670
Db	927	ACCCCCAGGATGGAGCCTGTTTCTGCCCTCCAGGGAGAGCAGGACCCAGCTGTAATGTGC	986
Qy	671	TTTGTCTCTCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGTCAAAATGGAG	730
Db	987	CCTGTTCACAGGGCACTGATGGCTTCTTCTGCCCCAGAACCTATCCTTGCCAAAATGGAG	1046
Qy	731	GAGTGTGTTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGATGGGCACAGTGT	790
Db	1047	GTGTTCCCTCAGGGCTCCCAAGGCTCCTGCAGCTGCCACCAGGGCTGGATGGGTGTCATTT	1106
Qy	791	GTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAATGCCAGTGCC	850
Db	1107	GTTCCCTGCCATGCCAGAGGGTTTCCATGGACCAACTGTACTCAGGAATGTCGCTGCC	1166
Qy	851	ATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCAGGATACACAG	910
Db	1167	ACAACGGTGGCCTCTGTGACAGGTTTACTGGGCAGTGCCACTGTGCTCCTGGCTATATCG	1226
Qy	911	GGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGTGCTGAGACCT	970
Db	1227	GGGATCGGTGCCAAGAAGAGTGCCCCGTGGGCCGCTTCGGTCAAGACTGTGCTGAGACCT	1286
Qy	971	GCCAGTGTGTCAACGGAGGGAAGTGTTACCACGTGAGCGGCGCATGCCTCTGTGAAGCAG	1030
Db	1287	GTGACTGTGCTCCTGGCGCCCGTTGCTTTCTGCTAATGGCGCGTGTCTGTGTGAACATG	1346
Qy	1031	GCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCTGAGGGGCTCTACGGCATCAAAT	1090
Db	1347	GCTTCACAGGCGACCGCTGCACTGAGCGCCTCTGTCCGGATGGCCGCTATGGTCTGAGCT	1406
Qy	1091	GTGACAAACGGTGTCCCTGCCACTTGGAAAACACTCATAGCTGTACCCCCATGTCTGGAG	1150
Db	1407	GCCAGGAGCCCTGCACCTGCGACCCAGAACACAGTCTCAGTGCACCCCGATGCACGGCG	1466
Qy	1151	AGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGTTCTCCTGGAT	1210
Db	1467	AGTGCTCCTGCCAGCCAGGTTGGGCGGGCCTCCACTGCAACGAGAGCTGCCCTCAGGACA	1526
Qy	1211	TCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTG	1270
Db	1527	CGCATGGCCCCGGCTGCCAGGAGCACTGCCTCTGTCTGCACGGAGGGCTCTGCCTTGCCG	1586
Qy	1271	TGACTGGAAAGTGACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACCCCATGCC	1330

Db	1587	ACAGCGCCTCTGCCGGTGCGCGCCGGGATACACGGGACCTCACTGCGCTAACCTATGTC	1646
Qy	1331	CTCTGGGAACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAATGATGCAGTCT	1390
Db	1647	CACCGGACACTTACGGGATCAACTGTTCTCCCGCTGCTCCTGTGAAAATGCCATTGCCT	1706
Qy	1391	GCTCTCCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCACGGGGTGGACTGCTCCA	1450
Db	1707	GCTCTCCCATCGACGGCACGTGCATCTGCAAGGAAGGTTGGCAGCGTGGTAACTGCTCTG	1766
Qy	1451	TCAGATGTCCAGTGGCACATGGGGCTTTGGCTGTAACTTAACATGCCAGTGCCTCAACG	1510
Db	1767	TTCCCTGTCCCTTGGCACCTGGGGCTTCAATTGCAATGCCAGTTGCCAGTGTGCCACG	1826
Qy	1511	GGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGGCGCGGGGAGA	1570
Db	1827	ACGGAGTCTGCAGCCCCAACTGGAGCCTGTACTTGACCCCTGGGTGGCATGGTGCTC	1886
Qy	1571	AATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAGCGCTGCGACT	1630
Db	1887	ACTGCCAGCTTCCCTGCCCGAAGGGACAGTTTGGTGAAGGCTGTGCCAGTGTCTGTGACT	1946
Qy	1631	GCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTCCCGGGATGGT	1690
Db	1947	GTGACCACTCTGATGGCTGTGACCCTGTTTCATGGACAGTGCCGATGTCAGGCTGGTTGGA	2006
Qy	1691	CAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAACTGCTCCCTGC	1750
Db	2007	TGGGCACACGTGCCACCTGCCTTGCCCGGAGGGCTTTTGGGGAGCCAACTGCAGTAACA	2066
Qy	1751	CCTGCTACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGCGAGTGTGCAC	1810
Db	2067	CCTGTACCTGCAAGAATGGTGGTACCTGTGTGTCTGAGAATGGCAACTGCGTGTGCGCAC	2126
Qy	1811	CAGGCTTCCGAGGCACCACTTGTGAGAGGATCTGCTCCCCTGGTTTTTATGGGCATCGCT	1870
Db	2127	CAGGGTTCCGAGGCCCTCCTGCCAGAGGCCCTGCCCGCCTGGTGCCTATGGCAAACGCT	2186
Qy	1871	GCAGCCAGACATGCCACAGTGCGTTTCACAGCAGCGGGCCCTGCCACCACATACCCGGCC	1930
Db	2187	GTGTGCA-----ATGCAAGTGTAACAACAACCATTCTTCCTGCCACCCATCGGACGGGA	2240
Qy	1931	TGTGTGACTGCTTGCCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGTCCAGTGGCA	1990
Db	2241	CCTGCTCCTGCCTGGCGGGCTGGACAGGCCCTGACTGCTCCGAGGCATGTCCCCAGGCC	2300
Qy	1991	GATTTGGGAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACCTGTAACCCCA	2050
Db	2301	ACTGGGGACTCAAATGCTCCCAACTCTGCCAGTGTTCATCATGGTGGGACCTGCCACCCCC	2360
Qy	2051	TTGACAGATCTTGTGAGTGTACCCCGTTGGATTGGCAGTGAAGTGTCTCAACCATGTC	2110
Db	2361	AGGATGGGAGCTGTATCTGCACGCCAGGCTGGACTGGACCCAAGTCTTGAAGGCTGCC	2420
Qy	2111	CACCTGCCCACTGGGGCCCCAACTGCATCCACACGTGCAACTGCCATAATGGAGCTTTCT	2170

Qy	299	AAAGCGGGGAAATGTGTGTCCCCACTGTGCTGATAAATGTGTCCATGGTTCGCTGTATTG	358
Db	529	AGAGCAGGGGGTTCTGTGTCCCGCTCTGTGCCCAGGAGTGTGTCCATGGCCGTTGTGTGG	588
Qy	359	CTCCAAACACCTGTCAAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCG	418
Db	589	CACCCAATCAGTGCCAATGTGTGCCAGGCTGGCGGGGCGACGACTGTTCCAGTGAGTGTG	648
Qy	419	ATGGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGT	478
Db	649	CCCCAGGAATGTGGGGGCCACAGTGTGACAAGCCCTGCAGCTGCGGCAACAACAGCTCGT	708
Qy	479	GCAACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGG	538
Db	709	GTGATCCCAAGAGTGGGGTATGTTCTTGCCCTTCTGGTCTGCAGCCCCGAAGTGCCTTC	768
Qy	539	ACCGCTGTGAGCAGGGCACCTATGGTAACGACTGTGCATCAGAGATGCCAGTGCCAGAATG	598
Db	769	AGCCCTGTACCCCTGGCTACTATGGCCCTGCCAGTTCGCTGCCAGTGCC--ATG	825
Qy	599	GAGCCACCTGCGACCACGTACGGGGGAATGCCGCTGCCACCAGGATACACCGGAGCCT	658
Db	826	GGGCACCCTGCGATCCCCAGACTGGAGCCTGCTTCTGCCCCGAGAGAGAACTGGGCCCCA	885
Qy	659	TCTGTGAGGATCTTTGTCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTT	718
Db	886	GCTGTGACGTGTCTCTGTTCCAGGGCACTTCTGGCTTCTTCTGCCCCAGCACCCATCCTT	945
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Qy	779	TGGGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAG	838
Db	1006	TGGGCACCATCTGCTCCCTGCCCTGCCAGAGGGCTTTACGGACCCAAGTCTCCAGG	1065
Qy	839	AATGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTC	898
Db	1066	AATGTCGCTGCCACAACGGCGGCCTCTGTGACCGATTCACTGGGCAGTGCCGCTGCGCTC	1125
Qy	899	CAGGATACACAGGGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCT	958
Db	1126	CGGGTTACACTGGGGATCGGTGCCGGGAGGAGTGCCCGGTGGGCGCTTTGGGCAGGACT	1185
Qy	959	GTGCTGAGACCTGCCAGTGTGTCAACGGAGGGAAGTGTACCACGTGAGCGGCGCATGCC	1018
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Qy	1019	TCTGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCTGAGGGGCTCT	1078
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Qy 1739 ACTGCTCCCTGCCCTGCTACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCT 1798
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RESULT 14

RATORFD

LOCUS RATORFD 660 bp mRNA linear ROD 09-AUG-1996

DEFINITION Rattus norvegicus (clone REM4) ORF mRNA, partial cds.

ACCESSION L41686

VERSION L41686.1 GI:780366

KEYWORDS monoclonal autoantibody.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 660)

AUTHORS Asakura,K., Pogulis,R.J., Pease,L.R. and Rodriguez,M.

TITLE A monoclonal autoantibody which promotes central nervous system
remyelination is highly polyreactive to multiple known and novel
antigens

JOURNAL J. Neuroimmunol. 65 (1), 11-19 (1996)

MEDLINE 96235155

PUBMED 8642059

COMMENT Original source text: Rattus norvegicus (strain Holzman) cDNA to
mRNA.

FEATURES

source

Location/Qualifiers

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mRNA

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CDS

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ORIGIN

Query Match 16.0%; Score 548.2; DB 10; Length 660;

Best Local Similarity 89.6%; Pred. No. 8.7e-158;

Matches 589; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 598 GGAGCCACCTGCGACCACGTACGGGGGAATGCCGCTGCCCACCAGGATACACCGGAGCC 657

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Qy      1198 TGTTCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGG 1254
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RESULT 15

AX079681

LOCUS AX079681 632 bp DNA linear PAT 22-FEB-2001

DEFINITION Sequence 425 from Patent WO0107611.

ACCESSION AX079681

VERSION AX079681.1 GI:13159250

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Baker,K.P., Goddard,A. and Wood,W.I.

TITLE Human polypeptides and methods for the use thereof
JOURNAL Patent: WO 0107611-A 425 01-FEB-2001;
Genentech, Inc. (US)

FEATURES Location/Qualifiers
source 1. .632
/organism="Homo sapiens"
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ORIGIN

Query Match 15.6%; Score 534.8; DB 6; Length 632;
Best Local Similarity 95.3%; Pred. No. 1.3e-153;
Matches 593; Conservative 0; Mismatches 24; Indels 5; Gaps 4;

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Job time : 13036 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 29, 2004, 23:13:51 ; Search time 1266 Seconds
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Title: US-10-092-390-1
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: geneseqn2003cs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	1049.4	30.7	1273	7	ABZ36212	Abz36212 Human sec

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	28	390	11.4	4508	9	ADD78266	Add78266	Human CGD
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	40	272	7.9	353	3	AAA41581	Aaa41581	Human sec
c	41	243	7.1	3493	4	ABL19878	Abl19878	Drosophil
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ALIGNMENTS

RESULT 1

AAD46318

ID AAD46318 standard; cDNA; 3423 BP.

XX

AC AAD46318;

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DT 27-JAN-2003 (first entry)

XX

DE Human EGF-family protein encoding cDNA #1.

XX

KW Human; EGF-family protein; novel human protein; NHP; drug discovery;

KW restriction fragment length polymorphism analysis; forensic biology;

KW toxicity; infectious disease; biological disorder; medical disorder;

KW mental disorder; gene therapy; gene; ss.

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Qy	241	CGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTGTCCTGGATTTTATGAA	300
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Qy	361	CCAAACACCTGTCAGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGAT	420
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Qy	421	GGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGC	480
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Qy	481	AACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGAC	540
Db	481	AACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGAC	540
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Qy	901	GGATACACAGGGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGT	960
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Qy	1861	GGGCATCGCTGCAGCCAGACATGCCACAGTGCCTTCACAGCAGCGGGCCCTGCCACCAC	1920
Db	1861	GGGCATCGCTGCAGCCAGACATGCCACAGTGCCTTCACAGCAGCGGGCCCTGCCACCAC	1920
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Qy	1981	CCCAGTGGCAGATTTGGGAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACC	2040
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Db	2041	TGTAACCCCATTTGACAGATCTTGTCTAGTGTACCCCGGTTGGATTGGCAGTGAAGTGTCT	2100
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Qy	2221	TACTGCACTCAGAGATGTCCTCTAGGGTTTTATGGAAAAGATTGTGCACTGATATGCCAA	2280
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Qy	2941	CCGGCTGACTGGAAACATGGCGGCTACCTCAACGAGCTCGGTGCTTTTGGACTTGACAGA	3000
Db	2941	 CCGGCTGACTGGAAACATGGCGGCTACCTCAACGAGCTCGGTGCTTTTGGACTTGACAGA	3000
Qy	3001	AGCTATATGGGAAAATCCTTAAAAGACCTGGGAAAGAATTCTGAATATAATTCAAGTAAC	3060
Db	3001	 AGCTATATGGGAAAATCCTTAAAAGACCTGGGAAAGAATTCTGAATATAATTCAAGTAAC	3060
Qy	3061	TGCTCCCTAAGCAGTTCTGAGAACCCATATGCCACTATTAAAGACCCACCTGTACTTATC	3120
Db	3061	 TGCTCCCTAAGCAGTTCTGAGAACCCATATGCCACTATTAAAGACCCACCTGTACTTATC	3120
Qy	3121	CCGAAAAGCTCAGAGTGTGGTTATGTGGAGATGAAATCGCCGGCACGAAGAGATTCCCCA	3180
Db	3121	 CCGAAAAGCTCAGAGTGTGGTTATGTGGAGATGAAATCGCCGGCACGAAGAGATTCCCCA	3180
Qy	3181	TATGCAGAGATCAATAACTCAACTTCAGCCAACAGGAATGTCTATGAAGTTGAACCTACA	3240
Db	3181	 TATGCAGAGATCAATAACTCAACTTCAGCCAACAGGAATGTCTATGAAGTTGAACCTACA	3240
Qy	3241	GTGAGTGT'TGTCCAAGGAGTATTTCAGCAATAATGGGCGTCTCTCCAGGATCCATATGAC	3300
Db	3241	 GTGAGTGT'TGTCCAAGGAGTATTTCAGCAATAATGGGCGTCTCTCCAGGATCCATATGAC	3300
Qy	3301	CTCCCAAAGAACAGTCACATCCCTTGTCATTATGACCTGCTGCCAGTCCGAGACAGTTCA	3360
Db	3301	 CTCCCAAAGAACAGTCACATCCCTTGTCATTATGACCTGCTGCCAGTCCGAGACAGTTCA	3360
Qy	3361	TCCTCCCCTAAGCAAGAGGACAGTGGAGGTAGCAGCAGCAACAGCAGCAGCAGTGA	3420
Db	3361	 TCCTCCCCTAAGCAAGAGGACAGTGGAGGTAGCAGCAGCAACAGCAGCAGCAGTGA	3420
Qy	3421	TGA 3423	
Db	3421	 TGA 3423	

ADE71243

ID ADE71243 standard; DNA; 7522 BP.

XX

AC ADE71243;

XX

DT 29-JAN-2004 (first entry)

XX

DE Novel human protein coding sequence #59.

XX

KW human; novel protein; drug; gene; ds.

XX

OS Homo sapiens.

XX

PN JP2002345493-A.

XX

PD 03-DEC-2002.

XX

PF 29-MAR-2001; 2002JP-00049046.

XX

PR 29-MAR-2001; 2001JP-00095524.

XX

PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.

XX

DR WPI; 2003-460885/44.

DR P-PSDB; ADE71305.

XX

PT A gene and a protein encoded by it, used in drugs.

XX

PS Claim 1; SEQ ID NO 60; 257pp; Japanese.

XX

CC The invention comprises the amino acid and coding sequences of novel
CC human proteins. The DNA and protein sequences of the invention are used
CC in drugs. The present DNA sequence encodes a novel human protein of the
CC invention.

XX

SQ Sequence 7522 BP; 2130 A; 1554 C; 1697 G; 2141 T; 0 U; 0 Other;

Query Match 100.0%; Score 3421.4; DB 9; Length 7522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGTTATTTCTTTGAACTCATGCCTGAGCTTTATTTGTTTATTGTTATGCCACTGGATT	60
Db	204	ATGGTTATTTCTTTGAACTCATGCCTGAGCTTTATTTGTTTATTGTTATGCCACTGGATT	263
Qy	61	GGGACAGCATCACCTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTAC	120
Db	264	GGGACAGCATCACCTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTAC	323
Qy	121	TCAGTGACTGTGCAAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGC	180
Db	324	TCAGTGACTGTGCAAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGC	383
Qy	181	ACTGACATTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCTAT	240
Db	384	ACTGACATTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCTAT	443

Qy	241	CGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTGTCCTGGATTTTATGAA	300
Db	444	CGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTGTCCTGGATTTTATGAA	503
Qy	301	AGCGGGGAAATGTGTGTCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTGCT	360
Db	504	AGCGGGGAAATGTGTGTCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTGCT	563
Qy	361	CCAAACACCTGTCAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGAT	420
Db	564	CCAAACACCTGTCAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGAT	623
Qy	421	GGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGC	480
Db	624	GGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGC	683
Qy	481	AACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGAC	540
Db	684	AACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGAC	743
Qy	541	CGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATGGA	600
Db	744	CGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATGGA	803
Qy	601	GCCACCTGCGACCACGTACGCGGGGAATGCCGCTGCCCACCAGGATACACCGGAGCCTTC	660
Db	804	GCCACCTGCGACCACGTACGCGGGGAATGCCGCTGCCCACCAGGATACACCGGAGCCTTC	863
Qy	661	TGTGAGGATCTTTGTCCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGT	720
Db	864	TGTGAGGATCTTTGTCCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGT	923
Qy	721	CAAAATGGAGGAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGATG	780
Db	924	CAAAATGGAGGAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGATG	983
Qy	781	GGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAA	840
Db	984	GGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAA	1043
Qy	841	TGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCA	900
Db	1044	TGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCA	1103
Qy	901	GGATACACAGGGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGT	960
Db	1104	GGATACACAGGGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGT	1163
Qy	961	GCTGAGACCTGCCAGTGTGTCAACGGAGGGAAGTGTTACCACGTGAGCGGCGCATGCCTC	1020
Db	1164	GCTGAGACCTGCCAGTGTGTCAACGGAGGGAAGTGTTACCACGTGAGCGGCGCATGCCTC	1223
Qy	1021	TGTGAAGCAGGCTTTGCTGGCGAGCGCTGCCAAGCACGCCTGTGTCTGAGGGGCTCTAC	1080
Db	1224	TGTGAAGCAGGCTTTGCTGGCGAGCGCTGCCAAGCACGCCTGTGTCTGAGGGGCTCTAC	1283
Qy	1081	GGCATCAAATGTGACAAACGGTGTCCTGCCACTTGGAACAACTCATAGCTGTCACCCC	1140

Db	1284	GGCATCAAATGTGACAAACGGTGTCCCTGCCACTTGGAAAACACTCATAGCTGTACCCC	1343
Qy	1141	ATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGT	1200
Db	1344	ATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGT	1403
Qy	1201	TCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGAC	1260
Db	1404	TCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGAC	1463
Qy	1261	TGTGACAGTGTGACTGGAAAGTGACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCT	1320
Db	1464	TGTGACAGTGTGACTGGAAAGTGACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCT	1523
Qy	1321	ACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCCCTCTCGCTGTGGCTGTAAAAAT	1380
Db	1524	ACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCCCTCTCGCTGTGGCTGTAAAAAT	1583
Qy	1381	GATGCAGTCTGCTCTCCTGTGGACGGGTCTTGTAAGGCAAGGCTGGCACGGGGTG	1440
Db	1584	GATGCAGTCTGCTCTCCTGTGGACGGGTCTTGTAAGGCAAGGCTGGCACGGGGTG	1643
Qy	1441	GACTGCTCCATCAGATGTCCAGTGGCACATGGGGCTTTGGCTGTAACCTAACATGCCAG	1500
Db	1644	GACTGCTCCATCAGATGTCCAGTGGCACATGGGGCTTTGGCTGTAACCTAACATGCCAG	1703
Qy	1501	TGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGG	1560
Db	1704	TGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGG	1763
Qy	1561	CGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAG	1620
Db	1764	CGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAG	1823
Qy	1621	CGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTC	1680
Db	1824	CGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTC	1883
Qy	1681	CCGGGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAAC	1740
Db	1884	CCCGGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAAC	1943
Qy	1741	TGCTCCCTGCCCTGCTACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGC	1800
Db	1944	TGCTCCCTGCCCTGCTACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGC	2003
Qy	1801	GAGTGTGCACCAGGCTTCCGAGGCACCACTTGTGAGAGGATCTGCTCCCCTGGTTTTTAT	1860
Db	2004	GAGTGTGCACCAGGCTTCCGAGGCACCACTTGTGAGAGGATCTGCTCCCCTGGTTTTTAT	2063
Qy	1861	GGGCATCGCTGCAGCCAGACATGCCACAGTGCCTTACAGCAGCGGGCCCTGCCACCAC	1920
Db	2064	GGGCATCGCTGCAGCCAGACATGCCACAGTGCCTTACAGCAGCGGGCCCTGCCACCAC	2123
Qy	1921	ATCACCGGCCTGTGTGACTGCTTGCCCTGGCTTACAGGCGCCCTCTGCAATGAAGTGTGT	1980

Db	2124	ATCACCGGCCTGTGTGACTGCTTGCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGT	2183
Qy	1981	CCCAGTGGCAGATTTGGGAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACC	2040
Db	2184	CCCAGTGGCAGATTTGGGAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACC	2243
Qy	2041	TGTAACCCCATTTGACAGATCTTGTCAAGTGTACCCCGTTGGATTGGCAGTGAAGTGTCT	2100
Db	2244	TGTAACCCCATTTGACAGATCTTGTCAAGTGTACCCCGTTGGATTGGCAGTGAAGTGTCT	2303
Qy	2101	CAACCATGTCCACCTGCCCCTGGGGCCCAACTGCATCCACACGTGCAACTGCCATAAT	2160
Db	2304	CAACCATGTCCACCTGCCCCTGGGGCCCAACTGCATCCACACGTGCAACTGCCATAAT	2363
Qy	2161	GGAGCTTTCTGCAGCGCCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTC	2220
Db	2364	GGAGCTTTCTGCAGCGCCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTC	2423
Qy	2221	TACTGCACTCAGAGATGTCCTCTAGGGTTTATGGAAAAGATTGTGCACTGATATGCCAA	2280
Db	2424	TACTGCACTCAGAGATGTCCTCTAGGGTTTATGGAAAAGATTGTGCACTGATATGCCAA	2483
Qy	2281	TGTCAAAACGGAGCTGACTGCGACCACATTTCTGGGCAGTGTACTTGCCGCACTGGATTC	2340
Db	2484	TGTCAAAACGGAGCTGACTGCGACCACATTTCTGGGCAGTGTACTTGCCGCACTGGATTC	2543
Qy	2341	ATGGGACGGCACTGTGAGCAGAAGTGCCCTTCAGGAACATATGGCTATGGCTGTGCGCCAG	2400
Db	2544	ATGGGACGGCACTGTGAGCAGAAGTGCCCTTCAGGAACATATGGCTATGGCTGTGCGCCAG	2603
Qy	2401	ATATGTGATTGTCTGAACAACTCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGC	2460
Db	2604	ATATGTGATTGTCTGAACAACTCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGC	2663
Qy	2461	CCCGGATGGAAGGGAGCGAGATGTGATCAAGCTGGTGTATCATAGTTGGAAATCTGAAC	2520
Db	2664	CCCGGATGGAAGGGAGCGAGATGTGATCAAGCTGGTGTATCATAGTTGGAAATCTGAAC	2723
Qy	2521	AGCTTAAGCCGAACCACTGCTCTCCCTGCTGATTCCTACCAGATCGGGGCCATTGCA	2580
Db	2724	AGCTTAAGCCGAACCACTGCTCTCCCTGCTGATTCCTACCAGATCGGGGCCATTGCA	2783
Qy	2581	GGCATCATCATTCTTGTCTAGTTGTTCTCTTCCTACTGGCATTGTTTATTATTTATAGA	2640
Db	2784	GGCATCATCATTCTTGTCTAGTTGTTCTCTTCCTACTGGCATTGTTTATTATTTATAGA	2843
Qy	2641	CACAAGCAGAAGGGAAAGGAATCAAGCATGCCAGCAGTTACCTACACCCCTGCTATGAGG	2700
Db	2844	CACAAGCAGAAGGGAAAGGAATCAAGCATGCCAGCAGTTACCTACACCCCTGCTATGAGG	2903
Qy	2701	GTCGTCAATGCAGATTATACCATTTTTCAGGAACCCCTTCCTCACAGCAATGGTGGAAACGCT	2760
Db	2904	GTCGTCAATGCAGATTATACCATTTTTCAGGAACCCCTTCCTCACAGCAATGGTGGAAACGCT	2963
Qy	2761	AATAGCCACTACTTCACCAATCCAGTTACCACACGCTCACCAGTGTGCCACATCCCCCT	2820
Db	2964	AATAGCCACTACTTCACCAATCCAGTTACCACACGCTCACCAGTGTGCCACATCCCCCT	3023

Qy	2821	CACGTCAACAACAGGGACAGGATGACTGTCACGAAGTCAAAAAACAATCAACTGTTTGTG	2880
Db	3024	CACGTCAACAACAGGGACAGGATGACTGTCACGAAGTCAAAAAACAATCAACTGTTTGTG	3083
Qy	2881	AATCTTAAAAATGTGAACCTGGGAAGAGAGGCCCTGTGGGGGACTGCACTGGGACATTG	2940
Db	3084	AATCTTAAAAATGTGAACCTGGGAAGAGAGGCCCTGTGGGGGACTGCACTGGGACATTG	3143
Qy	2941	CCGGCTGACTGGAAACATGGCGGCTACCTCAACGAGCTCGGTGCTTTTGGACTTGACAGA	3000
Db	3144	CCGGCTGACTGGAAACATGGCGGCTACCTCAACGAGCTCGGTGCTTTTGGACTTGACAGA	3203
Qy	3001	AGCTATATGGGAAAATCCTTAAAAGACCTGGGAAAGAATTCTGAATATAATTCAAGTAAC	3060
Db	3204	AGCTATATGGGAAAATCCTTAAAAGACCTGGGAAAGAATTCTGAATATAATTCAAGTAAC	3263
Qy	3061	TGCTCCCTAAGCAGTTCTGAGAACCCATATGCCACTATTAAAGACCCACCTGTACTTATC	3120
Db	3264	TGCTCCCTAAGCAGTTCTGAGAACCCATATGCCACTATTAAAGACCCACCTGTACTTATC	3323
Qy	3121	CCGAAAAGCTCAGAGTGTGGTTATGTGGAGATGAAATCGCCGGCACGAAGAGATTCCCCA	3180
Db	3324	CCGAAAAGCTCAGAGTGTGGTTATGTGGAGATGAAATCGCCGGCACGAAGAGATTCCCCA	3383
Qy	3181	TATGCAGAGATCAATAACTCAACTTCAGCCAACAGGAATGTCTATGAAGTTGAACCTACA	3240
Db	3384	TATGCAGAGATCAATAACTCAACTTCAGCCAACAGGAATGTCTATGAAGTTGAACCTACA	3443
Qy	3241	GTGAGTGTTGTCCAAGGAGTATTCAGCAATAATGGGCGTCTCTCCAGGATCCATATGAC	3300
Db	3444	GTGAGTGTTGTCCAAGGAGTATTCAGCAATAATGGGCGTCTCTCCAGGATCCATATGAC	3503
Qy	3301	CTCCCAAAGAACAGTCACATCCCTTGTCATTATGACCTGCTGCCAGTCCGAGACAGTTCA	3360
Db	3504	CTCCCAAAGAACAGTCACATCCCTTGTCATTATGACCTGCTGCCAGTCCGAGACAGTTCA	3563
Qy	3361	TCCTCCCCTAAGCAAGAGGACAGTGGAGGTAGCAGCAGCAACAGCAGCAGCAGCAGTGAA	3420
Db	3564	TCCTCCCCTAAGCAAGAGGACAGTGGAGGTAGCAGCAGCAACAGCAGCAGCAGCAGTGAA	3623
Qy	3421	TGA	3423
Db	3624	TGA	3626

RESULT 3

ADD18689

ID ADD18689 standard; DNA; 7522 BP.

XX

AC ADD18689;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human disease related protein DNA sequence SeqID120.

XX

KW human; disease state; cytostatic; antiinflammatory; ophthalmological;

KW antiarteriosclerotic; vulnerary; gene therapy;
 KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
 KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
 KW glucose transportation; catecholamine synthesis; iron transport;
 KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
 KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
 KW inflammatory condition; wound healing; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003018621-A2.
 XX
 PD 06-MAR-2003.
 XX
 PF 23-AUG-2002; 2002WO-GB003892.
 XX
 PR 23-AUG-2001; 2001GB-00020558.
 PR 05-OCT-2001; 2001GB-00024037.
 XX
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX
 PI Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
 XX
 DR WPI; 2003-290046/28.
 DR P-PSDB; ADD18688.
 XX
 PT New substantially purified polypeptide, useful for diagnosing or treating
 PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
 PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
 PT wound healing.
 XX
 PS Claim 27; SEQ ID NO 120; 424pp; English.
 XX
 CC This invention relates to novel human genes and gene product which are
 CC implicated in certain disease states. Compounds which modulate the
 CC proteins of the invention may have cytostatic, antiinflammatory,
 CC ophthalmological, antiarteriosclerotic or vulnerary activities. The
 CC sequences of the invention may be useful for gene therapy. The invention
 CC may be useful for diagnosing or treating a hypoxia-regulated condition,
 CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
 CC erythropoiesis, or the biological response to hypoxia conditions
 CC including processes such as glycolysis, gluconeogenesis, glucose
 CC transportation, catecholamine synthesis, iron transport or nitric oxide
 CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
 CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
 CC inflammatory conditions or wound healing. The present sequence is that of
 CC a disease related protein encoding DNA sequence of the invention.
 XX
 SQ Sequence 7522 BP; 2130 A; 1555 C; 1696 G; 2141 T; 0 U; 0 Other;

Query Match 99.9%; Score 3419.8; DB 9; Length 7522;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 3421; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGTTATTTCTTTGAACTCATGCCTGAGCTTTATTTGTTTATTGTTATGCCACTGGATT 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 204 ATGGTTATTTCTTTGAACTCATGCCTGAGCTTTATTTGTTTATTGTTATGCCACTGGATT 263

Qy	61	GGGACAGCATCACCTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTAC	120
Db	264	GGGACAGCATCACCTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTAC	323
Qy	121	TCAGTGACTGTGCAAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGC	180
Db	324	TCAGTGACTGTGCAAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGC	383
Qy	181	ACTGACATTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCTAT	240
Db	384	ACTGACATTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCTAT	443
Qy	241	CGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTGTCCTGGATTTTATGAA	300
Db	444	CGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTGTCCTGGATTTTATGAA	503
Qy	301	AGCGGGGAAATGTGTGTCCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTGCT	360
Db	504	AGCGGGGAAATGTGTGTCCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTGCT	563
Qy	361	CCAAACACCTGTCAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGAT	420
Db	564	CCAAACACCTGTCAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGAT	623
Qy	421	GGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGC	480
Db	624	GGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGC	683
Qy	481	AACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGAC	540
Db	684	AACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGAC	743
Qy	541	CGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATGGA	600
Db	744	CGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATGGA	803
Qy	601	GCCACCTGCGACCACGTACGGGGGAATGCCGCTGCCCACCAGGATACACCGGAGCCTTC	660
Db	804	GCCACCTGCGACCACGTACGGGGGAATGCCGCTGCCCACCAGGATACACCGGAGCCTTC	863
Qy	661	TGTGAGGATCTTTGTCCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGT	720
Db	864	TGTGAGGATCTTTGTCCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGT	923
Qy	721	CAAAATGGAGGAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGATG	780
Db	924	CAAAATGGAGGAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGATG	983
Qy	781	GGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAAGTGTCCCAAGAA	840
Db	984	GGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAAGTGTCCCAAGAA	1043
Qy	841	TGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCA	900
Db	1044	TGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCA	1103

Qy	901	GGATACACAGGGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGT	960
Db	1104	GGATACACAGGGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGT	1163
Qy	961	GCTGAGACCTGCCAGTGTGTCAACGGAGGGGAAGTGTACCACGTGAGCGGCGCATGCCTC	1020
Db	1164	GCTGAGACCTGCCAGTGTGTCAACGGAGGGGAAGTGTACCACGTGAGCGGCCCATGCCTC	1223
Qy	1021	TGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCTGAGGGGCTCTAC	1080
Db	1224	TGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCTGAGGGGCTCTAC	1283
Qy	1081	GGCATCAAATGTGACAAACGGTGTCCCTGCCACTTGGAACAACTCATAGCTGTCACCCC	1140
Db	1284	GGCATCAAATGTGACAAACGGTGTCCCTGCCACTTGGAACAACTCATAGCTGTCACCCC	1343
Qy	1141	ATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGT	1200
Db	1344	ATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGT	1403
Qy	1201	TCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGAC	1260
Db	1404	TCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGAC	1463
Qy	1261	TGTGACAGTGTGACTGGAAAGTGACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCT	1320
Db	1464	TGTGACAGTGTGACTGGAAAGTGACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCT	1523
Qy	1321	ACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAAT	1380
Db	1524	ACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAAT	1583
Qy	1381	GATGCAGTCTGCTCTCCTGTGGACGGGTCTTGTAAGTGGCAAGGCAGGCTGGCACGGGGTG	1440
Db	1584	GATGCAGTCTGCTCTCCTGTGGACGGGTCTTGTAAGTGGCAAGGCAGGCTGGCACGGGGTG	1643
Qy	1441	GACTGCTCCATCAGATGTCCAGTGGCACATGGGGCTTTGGCTGTAACTTAACATGCCAG	1500
Db	1644	GACTGCTCCATCAGATGTCCAGTGGCACATGGGGCTTTGGCTGTAACTTAACATGCCAG	1703
Qy	1501	TGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGG	1560
Db	1704	TGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGG	1763
Qy	1561	CGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAG	1620
Db	1764	CGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAG	1823
Qy	1621	CGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGGCCATTGCCGCTGCCTC	1680
Db	1824	CGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGGCCATTGCCGCTGCCTC	1883
Qy	1681	CCGGGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAAC	1740
Db	1884	CCCGGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAAC	1943
Qy	1741	TGCTCCCTGCCCTGCTACTGTAAAAATGGGGCTTCATGCTCCCTGATGATGGCATCTGC	1800

Db	1944	 TGCTCCCTGCCCTGCTACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGC	2003
Qy	1801	GAGTGTGCACCAGGCTTCCGAGGCACCACTTGTGAGGATCTGCTCCCCTGGTTTTTAT	1860
Db	2004	 GAGTGTGCACCAGGCTTCCGAGGCACCACTTGTGAGGATCTGCTCCCCTGGTTTTTAT	2063
Qy	1861	GGGCATCGCTGCAGCCAGACATGCCCACAGTGCCTTCACAGCAGCGGGCCCTGCCACCAC	1920
Db	2064	 GGGCATCGCTGCAGCCAGACATGCCCACAGTGCCTTCACAGCAGCGGGCCCTGCCACCAC	2123
Qy	1921	ATCACCGGCCTGTGTGACTGCTTGCCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGT	1980
Db	2124	 ATCACCGGCCTGTGTGACTGCTTGCCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGT	2183
Qy	1981	CCCAGTGGCAGATTTGGGAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACC	2040
Db	2184	 CCCAGTGGCAGATTTGGGAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACC	2243
Qy	2041	TGTAACCCCATTTGACAGATCTTGTGAGTGTACCCCGGTTGGATTGGCAGTGACTGCTCT	2100
Db	2244	 TGTAACCCCATTTGACAGATCTTGTGAGTGTACCCCGGTTGGATTGGCAGTGACTGCTCT	2303
Qy	2101	CAACCATGTCCACCTGCCCACTGGGGCCCAAAGTGCATCCACACGTGCAACTGCCATAAT	2160
Db	2304	 CAACCATGTCCACCTGCCCACTGGGGCCCAAAGTGCATCCACACGTGCAACTGCCATAAT	2363
Qy	2161	GGAGCTTTCTGCAGCGCCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTC	2220
Db	2364	 GGAGCTTTCTGCAGCGCCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTC	2423
Qy	2221	TACTGCACTCAGAGATGTCCTCTAGGGTTTTATGGAAAAGATTGTGCACTGATATGCCAA	2280
Db	2424	 TACTGCACTCAGAGATGTCCTCTAGGGTTTTATGGAAAAGATTGTGCACTGATATGCCAA	2483
Qy	2281	TGTCAAAACGGAGCTGACTGCGACCACATTTCTGGGCAGTGTACTTGCCGCACTGGATTTC	2340
Db	2484	 TGTCAAAACGGAGCTGACTGCGACCACATTTCTGGGCAGTGTACTTGCCGCACTGGATTTC	2543
Qy	2341	ATGGGACGGCACTGTGAGCAGAAGTGCCCTTCAGGAACATATGGCTATGGCTGTCGCCAG	2400
Db	2544	 ATGGGACGGCACTGTGAGCAGAAGTGCCCTTCAGGAACATATGGCTATGGCTGTCGCCAG	2603
Qy	2401	ATATGTGATTGTCTGAACAACTCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGC	2460
Db	2604	 ATATGTGATTGTCTGAACAACTCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGC	2663
Qy	2461	CCCGGATGGAAGGGAGCGAGATGTGATCAAGCTGGTGTATCATAGTTGGAAATCTGAAC	2520
Db	2664	 CCCGGATGGAAGGGAGCGAGATGTGATCAAGCTGGTGTATCATAGTTGGAAATCTGAAC	2723
Qy	2521	AGCTTAAGCCGAACCACTGCTCTCCCTGCTGATTTCCTACCAGATCGGGGCCATTGCA	2580
Db	2724	 AGCTTAAGCCGAACCACTGCTCTCCCTGCTGATTTCCTACCAGATCGGGGCCATTGCA	2783
Qy	2581	GGCATCATCATTCTTGTCTAGTTGTTCTCTTCCCTACTGGCATTGTTTATTATATAGA	2640

Db	2784	GGCATCATCATTCTTGTCTAGTTGTTCTCTTCTACTGGCATTGTTTCATTATTTATAGA	2843
Qy	2641	CACAAGCAGAAGGGAAAGGAATCAAGCATGCCAGCAGTTACCTACACCCCTGCTATGAGG	2700
Db	2844	CACAAGCAGAAGGGAAAGGAATCAAGCATGCCAGCAGTTACCTACACCCCTGCTATGAGG	2903
Qy	2701	GTCGTCAATGCAGATTATACCATTTTCAGGAACCCCTTCCTCACAGCAATGGTGGAAACGCT	2760
Db	2904	GTCGTCAATGCAGATTATACCATTTTCAGGAACCCCTTCCTCACAGCAATGGTGGAAACGCT	2963
Qy	2761	AATAGCCACTACTTCACCAATCCCAGTTACCACACGCTCACCCAGTGTGCCACATCCCCT	2820
Db	2964	AATAGCCACTACTTCACCAATCCCAGTTACCACACGCTCACCCAGTGTGCCACATCCCCT	3023
Qy	2821	CACGTCAACAACAGGGACAGGATGACTGTCACGAAGTCAAAAAACAATCAACTGTTTGTG	2880
Db	3024	CACGTCAACAACAGGGACAGGATGACTGTCACGAAGTCAAAAAACAATCAACTGTTTGTG	3083
Qy	2881	AATCTTAAAAATGTGAACCCTGGGAAGAGAGGCCCTGTGGGGGACTGCACTGGGACATTG	2940
Db	3084	AATCTTAAAAATGTGAACCCTGGGAAGAGAGGCCCTGTGGGGGACTGCACTGGGACATTG	3143
Qy	2941	CCGGCTGACTGGAAACATGGCGGCTACCTCAACGAGCTCGGTGCTTTTGGACTTGACAGA	3000
Db	3144	CCGGCTGACTGGAAACATGGCGGCTACCTCAACGAGCTCGGTGCTTTTGGACTTGACAGA	3203
Qy	3001	AGCTATATGGGAAAATCCTTAAAAGACCTGGGAAAGAATTCTGAATATAATTCAAGTAAC	3060
Db	3204	AGCTATATGGGAAAATCCTTAAAAGACCTGGGAAAGAATTCTGAATATAATTCAAGTAAC	3263
Qy	3061	TGCTCCCTAAGCAGTTCTGAGAACCCATATGCCACTATTAAAGACCCACCTGTACTTATC	3120
Db	3264	TGCTCCCTAAGCAGTTCTGAGAACCCATATGCCACTATTAAAGACCCACCTGTACTTATC	3323
Qy	3121	CCGAAAAGCTCAGAGTGTGGTTATGTGGAGATGAAATCGCCGGCACGAAGAGATTCCCCA	3180
Db	3324	CCGAAAAGCTCAGAGTGTGGTTATGTGGAGATGAAATCGCCGGCACGAAGAGATTCCCCA	3383
Qy	3181	TATGCAGAGATCAATAACTCAACTTCAGCCAACAGGAATGTCTATGAAGTTGAACCTACA	3240
Db	3384	TATGCAGAGATCAATAACTCAACTTCAGCCAACAGGAATGTCTATGAAGTTGAACCTACA	3443
Qy	3241	GTGAGTGTTGTCCAAGGAGTATTTCAGCAATAATGGGCGTCTCTCCCAGGATCCATATGAC	3300
Db	3444	GTGAGTGTTGTCCAAGGAGTATTTCAGCAATAATGGGCGTCTCTCCCAGGATCCATATGAC	3503
Qy	3301	CTCCCAAAGAACAGTCACATCCCTTGTTCATTATGACCTGCTGCCAGTCCGAGACAGTTCA	3360
Db	3504	CTCCCAAAGAACAGTCACATCCCTTGTTCATTATGACCTGCTGCCAGTCCGAGACAGTTCA	3563
Qy	3361	TCCTCCCCTAAGCAAGAGGACAGTGGAGGTAGCAGCAGCAACAGCAGCAGCAGTGA	3420
Db	3564	TCCTCCCCTAAGCAAGAGGACAGTGGAGGTAGCAGCAGCAACAGCAGCAGCAGTGA	3623
Qy	3421	TGA	3423
Db	3624	TGA	3626

RESULT 4

AAD46319

ID AAD46319 standard; cDNA; 1761 BP.

XX

AC AAD46319;

XX

DT 27-JAN-2003 (first entry)

XX

DE Human EGF-family protein encoding cDNA #2.

XX

KW Human; EGF-family protein; novel human protein; NHP; drug discovery;

KW restriction fragment length polymorphism analysis; forensic biology;

KW toxicity; infectious disease; biological disorder; medical disorder;

KW mental disorder; gene therapy; gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .1761

FT /*tag= a

FT /product= "Human EGF-family protein #2"

XX

PN WO200272611-A2.

XX

PD 19-SEP-2002.

XX

PF 06-MAR-2002; 2002WO-US007477.

XX

PR 12-MAR-2001; 2001US-0275013P.

XX

PA (LEXI-) LEXICON GENETICS INC.

XX

PI Yu X, Miranda M;

XX

DR WPI; 2002-723315/78.

DR P-PSDB; AAE27986.

XX

PT New novel human nucleic acids useful for e.g. identifying protein coding

PT sequences and mapping unique genes to a particular chromosome, as DNA

PT markers for restriction fragment length polymorphism analysis, or in

PT forensic biology.

XX

PS Disclosure; Page 40; 42pp; English.

XX

CC The present sequence is a cDNA encoding human EGF-family protein, a novel

CC human protein (NHP). The NHP sequences are useful for mapping unique

CC genes to a particular chromosome; as DNA markers for restriction fragment

CC length polymorphism analysis; in forensic biology; in defining and

CC monitoring both drug action and toxicity; in identifying, selecting and

CC validating novel molecular targets for drug discovery; in microarrays or

CC other assay formats to screen collections of genetic material from

CC patients who have a particular medical condition. The NHP peptides,

CC fusion proteins, antibodies, antagonists and agonists can be used for

CC detecting mutant NHPs or inappropriately expressed NHPs for the diagnosis

CC of disease; for screening drugs for treatment of symptomatic or

CC phenotypic manifestations of perturbing the normal function of NHP in the
CC body and to treat diseases including infectious, mental, biological, or
CC medical diseases or disorders. They are also used in gene therapy
XX
SQ Sequence 1761 BP; 370 A; 465 C; 525 G; 401 T; 0 U; 0 Other;

Query Match 51.4%; Score 1760; DB 6; Length 1761;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1760; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 ATGGTTATTTCTTTGAACTCATGCCTGAGCTTTATTTGTTTATTGTTATGCCACTGGATT 60
          |||
Db      1 ATGGTTATTTCTTTGAACTCATGCCTGAGCTTTATTTGTTTATTGTTATGCCACTGGATT 60

Qy     61 GGGACAGCATCACCTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTAC 120
          |||
Db     61 GGGACAGCATCACCTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTAC 120

Qy    121 TCAGTGACTGTGCAAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGC 180
          |||
Db    121 TCAGTGACTGTGCAAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGC 180

Qy    181 ACTGACATTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCTAT 240
          |||
Db    181 ACTGACATTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCTAT 240

Qy    241 CGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTCCTGGATTTTATGAA 300
          |||
Db    241 CGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTCCTGGATTTTATGAA 300

Qy    301 AGCGGGGAAATGTGTGTCCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTGCT 360
          |||
Db    301 AGCGGGGAAATGTGTGTCCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTGCT 360

Qy    361 CCAAACACCTGTCAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGAT 420
          |||
Db    361 CCAAACACCTGTCAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGAT 420

Qy    421 GGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGC 480
          |||
Db    421 GGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGC 480

Qy    481 AACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGAC 540
          |||
Db    481 AACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGAC 540

Qy    541 CGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATGGA 600
          |||
Db    541 CGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATGGA 600

Qy    601 GCCACCTGCGACCACGTCACGGGGGAATGCCGCTGCCACCAGGATACACCGGAGCCTTC 660
          |||
Db    601 GCCACCTGCGACCACGTCACGGGGGAATGCCGCTGCCACCAGGATACACCGGAGCCTTC 660

Qy    661 TGTGAGGATCTTTGTCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGT 720
          |||
Db    661 TGTGAGGATCTTTGTCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGT 720
```

Qy	721	CAAAATGGAGGAGTGTGTATCACGTCCTGGAGAATGCTCTTGCCCTTCTGGCTGGATG	780
Db	721	CAAAATGGAGGAGTGTGTATCACGTCCTGGAGAATGCTCTTGCCCTTCTGGCTGGATG	780
Qy	781	GGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAA	840
Db	781	GGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAA	840
Qy	841	TGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCA	900
Db	841	TGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCA	900
Qy	901	GGATACACAGGGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGT	960
Db	901	GGATACACAGGGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGT	960
Qy	961	GCTGAGACCTGCCAGTGTGTCAACGGAGGGAAAGTGTACCACGTGAGCGGCGCATGCCTC	1020
Db	961	GCTGAGACCTGCCAGTGTGTCAACGGAGGGAAAGTGTACCACGTGAGCGGCGCATGCCTC	1020
Qy	1021	TGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCCTGAGGGGCTCTAC	1080
Db	1021	TGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCCTGAGGGGCTCTAC	1080
Qy	1081	GGCATCAAATGTGACAAACGGTGTCCCTGCCACTTGAAAAACACTCATAGCTGTCACCCC	1140
Db	1081	GGCATCAAATGTGACAAACGGTGTCCCTGCCACTTGAAAAACACTCATAGCTGTCACCCC	1140
Qy	1141	ATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGT	1200
Db	1141	ATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGT	1200
Qy	1201	TCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGAC	1260
Db	1201	TCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGAC	1260
Qy	1261	TGTGACAGTGTGACTGGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCT	1320
Db	1261	TGTGACAGTGTGACTGGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCT	1320
Qy	1321	ACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCCCTCTCGCTGTGGCTGTAAAAAT	1380
Db	1321	ACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCCCTCTCGCTGTGGCTGTAAAAAT	1380
Qy	1381	GATGCAGTCTGCTCTCCTGTGGACGGGTCTTGACTTGCAAGGCAGGCTGGCACGGGGTG	1440
Db	1381	GATGCAGTCTGCTCTCCTGTGGACGGGTCTTGACTTGCAAGGCAGGCTGGCACGGGGTG	1440
Qy	1441	GACTGCTCCATCAGATGTCCCAGTGGCACATGGGGCTTTGGCTGTAACCTAACATGCCAG	1500
Db	1441	GACTGCTCCATCAGATGTCCCAGTGGCACATGGGGCTTTGGCTGTAACCTAACATGCCAG	1500
Qy	1501	TGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGG	1560
Db	1501	TGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGG	1560

Qy	1561	CGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGGCTGAACTGTGCTGAG	1620
Db	1561	CGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGGCTGAACTGTGCTGAG	1620
Qy	1621	CGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTC	1680
Db	1621	CGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTC	1680
Qy	1681	CCGGGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAAC	1740
Db	1681	CCGGGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAAC	1740
Qy	1741	TGCTCCCTGCCCTGCTACTG	1760
Db	1741	TGCTCCCTGCCCTGCTACTG	1760

RESULT 5

AAS72220

ID AAS72220 standard; cDNA; 2909 BP.

XX

AC AAS72220;

XX

DT 13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #8024.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

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OS Homo sapiens.

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PN WO200175067-A2.

XX

PD 11-OCT-2001.

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PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX

DR WPI; 2001-639362/73.

DR P-PSDB; ABG08033.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity.

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PS Claim 1; SEQ ID NO 8024; 103pp; English.

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CC The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridisation probes, polymerase chain

Qy 1610 ACTGTGCTGAGCGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATT 1669
 |||
 Db 575 ACTGTGCTGAGCGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATT 634

Qy 1670 GCCGCTGCCTCCCGGGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCT 1729
 |||
 Db 635 GCCGCTGCCTCCCGGGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCT 694

Qy 1730 GGGGCCCCAACTGCTCCCTGCCCTGCTACTGTAAAAATGGGGCTTCATGCTCCCTGATG 1789
 |||
 Db 695 GGGGCCCCAACTGCTCCCTGCCCTGCTACTGTAAAAATGGGGCTTCATGCTCCCTGATG 754

Qy 1790 ATGGCATCTGCGAGTGTGCACCAGGCTTCCGAGGCACCACTTGTGAGAGGATCTGCTCCC 1849
 |||
 Db 755 ATGGCATCTGCGAGTGTGCACCAGGCTTCCGAGGCACCACTTGTGAGAGGATCTGCTCCC 814

Qy 1850 CTGGTTTTTATGGGCATCGCTGCAGCCAGACATGCCCACAGTGCCTTCACAGCAGCGGGC 1909
 |||
 Db 815 CTGGTTTTTATGGGCATCGCTGCAGCCAGACATGCCCACAGTGCCTTCACAGCAGCGGGC 874

Qy 1910 CCTGCCACCACATCACCAGGCTGTGTGACTGCTTGCCTGGCTTCACAGGCGCCCTCTGCA 1969
 |||
 Db 875 CCTGCCACCACATCACCAGGCTGTGTGACTGCTTGCCTGGCTTCACAGGCGCCCTCTGCA 934

Qy 1970 ATGA-----AGTGTGTCCCAGTGGCAGATTTGGGAAAACTGTGCAGGAATTTG 2018
 |||
 Db 935 ATGAAGCTTATTCACAGTGTGTCCCAGTGGCAGATTTGGGAAAACTGTGCAGGAATTTG 994

Qy 2019 TACCTGCACCAACAACGGAACCTGTAACCCCATTGACAGATCTTGTGAGTGTACCCCGG 2078
 |||
 Db 995 TACCTGCACCAACAACGGAACCTGTAACCCCATTGACAGATCTTGTGAGTGTACCCCGG 1054

Qy 2079 TTGGATTGGCAGTGACTGCTCTCAACCATGTCCACCTGCCCACTGGGGCCCAAACCTGCAT 2138
 |||
 Db 1055 TTGGATTGGCAGTGACTGCTCTCAACCATGTCCACCTGCCCACTGGGGCCCAAACCTGCAT 1114

Qy 2139 CCACACGTGCAACTGCCATAATGGAGCTTTCTGCAGCGCTACGATGGGGAATGTAAATG 2198
 |||
 Db 1115 CCACACGTGCAACTGCCATAATGGAGCTTTCTGCAGCGCTACGATGGGGAATGTAAATG 1174

Qy 2199 CACTCCTGGCTGGACAGGGCTCTACTGCACTCAGAGATGTCC----- 2240
 |||
 Db 1175 CACTCCTGGCTGGACAGGGCTCTACTGCACTCAGAAGATCCCCAAGACACTCTTGCAGGG 1234

Qy 2241 -----TCTAGGGTTTTATGGAAAAGATTGTGCACTGATATGCCAATGTCAAAACG 2290
 |||
 Db 1235 CAGCTGCCAGCCCATGGTTTTATGGAAAAGATTGTGCACTGATATGCCAATGTCAAAACG 1294

Qy 2291 GAGCTGACTGCGACCACATTTCTGGGCAGTGTACTTGCCGCACTGGATTTCATGGGACGGC 2350
 |||
 Db 1295 GAGCTGACTGCGACCACATTTCTGGGCAGTGTACTTGCCGCACTGGATTTCATGGGACGGC 1354

Qy 2351 ACTGTGAGCAGA----- 2362
 |||
 Db 1355 ACTGTGAGCAGAAGGTCAGGCCTCCCTGGGATCATCGCTGGTTACTCACTGCTCTGGGCG 1414

Qy 2363 ----- 2362

Db 1415 GAGGAGGTGTGACTACAAGAATGAAGACAGAATTCAAGTTTCCATTCTGTTCTTTTGGG 1474

Qy 2363 ----- 2362

Db 1475 CTCTCCCTTCCTCTCCTTCTTATTTTTGGAATGTGGCTGCTCAGAGCCTTAAAAGATCCA 1534

Qy 2363 ----- 2362

Db 1535 GTCGAGCTTTCTTCATGGCAGAGGCAGAACCCGGGTCTCACATTGGAGGACAGTACATTC 1594

Qy 2363 ----- 2362

Db 1595 GGTGGGGAGGAGGGCTGGTGGCCCAGGGCCAATCCCTGTTGCTGCCCTGTGCAGTCTGGA 1654

Qy 2363 ----- 2362

Db 1655 CTGTGAGTGCCACCATGATTCCAGGAATGCTGTCCAGTTCTGGGACACTCTTGGGGGTAC 1714

Qy 2363 ----- 2362

Db 1715 AAGTCAGCCTCAATAGGAATCCCCTGAAAGGACTCAGCTCTAGATGTGCAGGGCTTGCAG 1774

Qy 2363 ----- 2362

Db 1775 TCAGAGACAGCCTTGCTCCAAATCCCAAGGTTGGAAAGCTACATTTGACTTTCTTCTC 1834

Qy 2363 ---AGTGCCCTTCAGGAACATATGGCTATGGCTGTGCCAGATATGTGATTGTCTGAACA 2419
 |||

Db 1835 TAGAGTGCCCTTCAGGAACATATGGCTATGGCTGTGCCAGATATGTGATTGTCTGAACA 1894

Qy 2420 ACTCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGCCCCGGATGGAAGGGAGCGA 2479
 |||

Db 1895 ACTCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGCCCCGGATGGAAGGGAGCGA 1954

Qy 2480 GATGTGATCAAGCTGGTGTATCATAGTTGGAATCTGAACAGCTTAAGCCGAACCAGTA 2539
 |||

Db 1955 GATGTGATCAAGCTGGTGTATCATAGTTGGAATCTGAACAGCTTAAGCCGAACCAGTA 2014

Qy 2540 CTGCTCTCCCTGCTGATTCCCTACCAGATCGGGGCCATTGCAGGCATCATCATTCTTGTCC 2599
 |||

Db 2015 CTGCTCTCCCTGCTGATTCCCTACCAGATCGGGGCCATTGCAGGCATCATCATTCTTGTCC 2074

Qy 2600 TAGTTGTTCTCTTCCTACTGGCATTGTTCAATTATTTATAGACACAAGCAGAAGGGAAAGG 2659
 |||

Db 2075 TAGTTGTTCTCTTCCTACTGGCATTGTTCAATTATTTATAGACACAAGCAGAAGGGAAAGG 2134

Qy 2660 AATCAAGCATGCCAGCAGTTACCTACACCCCTGCTATGAGGGTCGTCAATGCAGATTATA 2719
 |||

Db 2135 AATCAAGCATGCCAGCAGTTACCTACACCCCTGCTATGAGGGTCGTCAATGCAGATTATA 2194

Qy 2720 CCATTTTCAGGAACCCCTTCCTCACAGCAATGGTGGAAACGCTAATAGCCACTACTTCACCA 2779
 |||

Db 2195 CCATTTTCAGGAACCCCTTCCTCACAGCAATGGTGGAAACGCTAATAGCCACTACTTCACCA 2254

Qy 2780 ATCCCAGTTACCACACGCTCACCCAGTGTGCCACATCCCCT---CACGTCAACAACAGGG 2836

Db	2255		ATCCCAGTTACACACGCTCACCCAGTGTGCCACATCCCCTTCACGTTCAACAACAGGGG	2314
Qy	2837		ACAGGATGACTG-TCACGAAGTCAAAAAACAATCAACTGTTTGTGAATCTTAAAAATGTG	2895
Db	2315		ACAGGATGACTGTTACAGAGTTCAAAAACAATCAACTGTTTGTGAATCTTAAAAATGTG	2374
Qy	2896		AACCCTGGGAAGAGAGGCCCTGT-GGGGGACTGCACTGGGACATTGCCGGCTGACTGGAA	2954
Db	2375		AACCCTGGGAAGAGAGGCCCTGTGGGGGACTGCACTGGGACATTGCCGGCTGACTGGAA	2434
Qy	2955		ACATGGCGGCTACCTCAACGAGCT--CGGTGCTTTTGGACTTGACAGAAGCTATAT-GGG	3011
Db	2435		ACATGGCGGCTACCTCAACGAGCTTCGGTGCTTTTGGGACTTGACAGAAGCTATTTGGGG	2494
Qy	3012		AAAATCCTTAAAAGACC---TGGGAAAGAATTCTGAATATAATTCAAGTAAGTCTCCCT	3068
Db	2495		AAAATCCTTAAAAGGACCTGGGGAAGGATTTTGAATATAATTCAAGTAAGTCTCCCT	2554
Qy	3069		AAGCAGTTCTGAGAACCCATATGCCACTATTAAAGACCCACCTGTACTTATCCCGAAAAG	3128
Db	2555		AAGCAGTTCTGAGAACCCATATGCCACTATTAAAGACCCACCTGTACTTATCCCGAAAAG	2614
Qy	3129		CTCAGAGTGTGGTTATGTGGAGATGAAATCGCCGGGCACGAAGAGATTCCCCATATGCAGA	3188
Db	2615		CTCAGAGTGTGGTTATGTGGAGATGAAATCGCCGGGCACGAAGAGATTCCCCATATGCAGA	2674
Qy	3189		GATCAATAACTCAACTTCAGCCAACAGGAATGTCTATGAAGTTGAACCTACAGTGAGTGT	3248
Db	2675		GATCAATAACTCAACTTCAGCCAACAGGAATGTCTATGAAGTTGAACCTACAGTGAGTGT	2734
Qy	3249		TGTCCAAGGAGTATTCAGCAATAATGGGCGTCTCTCCCAGGATCCATATGACCTCCCAA	3308
Db	2735		TGTCCAAGGAGTATTCAGCAATAATGGGCGTCTCTCCCAGGATCCATATGACCTCCCAA	2794
Qy	3309		GAACAGTCACATCCCTTGTCATTATGACCTGCTGCCAGTCCGAGACAGTTCATCCTCCCC	3368
Db	2795		GAACAGTCACATCCCTTGTCATTATGACCTGCTGCCAGTCCGAGACAGTTCATCCTCCCC	2854
Qy	3369		TAAGCAAGAGGACAGTGGAGGTAGCAGCAGCAACAGCAGCAGCAGCAGTGAATGA	3423
Db	2855		TAAGCAAGAGGACAGTGGTGGTAGCAGCAGCAACAGCAGCAGCAGCAGTGAATGA	2909

RESULT 6

AAX19959

ID AAX19959 standard; DNA; 1448 BP.

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AC AAX19959;

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DT 15-JUN-1999 (first entry)

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DE Human Tango-83 5'-portion.

XX

KW Human; Tango-71; Tango-73; Tango-74; Tango-76; Tango-83; diagnosis;

KW detection; ds.

XX

OS Homo sapiens.
 XX
 PN WO9907850-A1.
 XX
 PD 18-FEB-1999.
 XX
 PF 06-AUG-1998; 98WO-US016502.
 XX
 PR 06-AUG-1997; 97US-0054966P.
 PR 05-SEP-1997; 97US-0058108P.
 XX
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 XX
 PI Holtzman DA, Goodearl ADJ;
 XX
 DR WPI; 1999-167426/14.
 XX
 PT New TANGO polypeptides and nucleic acids encoding them - useful as
 PT diagnostic agents and for treating disorders caused by aberrant
 PT expression of TANGO.
 XX
 PS Claim 1; Fig 7; 84pp; English.
 XX
 CC The present sequence is a 5'-portion of Tango-83. Tango polypeptides are
 CC useful for identifying compounds which bind the polypeptide via direct
 CC binding, competition binding assays or Tango-71, -73, -74, 76 or -83-
 CC mediated signal transduction. Tango polypeptides are also useful for
 CC identifying modulating compounds by determining effect on Tango activity.
 CC Tango polypeptides and nucleic acids are useful for diagnosing diseases
 CC related to aberrant expression of Tango, and Tango polypeptides are
 CC useful for raising antibodies which can be used in diagnostic assays for
 CC detection of Tango, and also for generating anti-idiotypic antibodies for
 CC prevention and protection
 XX
 SQ Sequence 1448 BP; 308 A; 407 C; 400 G; 333 T; 0 U; 0 Other;

 Query Match 41.7%; Score 1425.8; DB 2; Length 1448;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1427; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 Qy 1216 GGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTGTGACT 1275
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 18 GGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTGTGACT 77

 Qy 1276 GGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACCCCATGCCCTCTG 1335
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 78 GGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACCCCATGCCCTCTG 137

 Qy 1336 GGAACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAATGATGCAGTCTGCTCT 1395
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 138 GGAACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAATGATGCAGTCTGCTCT 197

 Qy 1396 CCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCACGGGGTGGACTGCTCCATCAGA 1455
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 198 CCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCACGGGGTGGACTGCTCCATCAGA 257

 Qy 1456 TGTCCCAGTGGCACATGGGGCTTTGGCTGTAACTTAACATGCCAGTGCCTCAACGGGGGA 1515

Db	258	TGTCCAGTGGCACATGGGGCTTTGGCTGTAACCTAACATGCCAGTGCCTCAACGGGGGA	317
Qy	1516	GCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGGCGCGGGGAGAAATGC	1575
Db	318	GCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGGCGCGGGGAGAAATGC	377
Qy	1576	GAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACCTGTGCTGAGCGCTGCGACTGCAGC	1635
Db	378	GAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACCTGTGCTGAGCGCTGCGACTGCAGC	437
Qy	1636	CACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTCCCGGGATGGTCAGGT	1695
Db	438	CACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTCCCGGGATGGTCAGGT	497
Qy	1696	GTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAACTGCTCCCTGCCCTGC	1755
Db	498	GTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAACTGCTCCCTGCCCTGC	557
Qy	1756	TACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGCGAGTGTGCACCAGGC	1815
Db	558	TACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGCGAGTGTGCACCAGGC	617
Qy	1816	TTCCGAGGCACCACTTGTGAGAGGATCTGCTCCCCTGGTTTTATGGGCATCGCTGCAGC	1875
Db	618	TTCCGAGGCACCACTTGTGAGAGGATCTGCTCCCCTGGTTTTATGGGCATCGCTGCAGC	677
Qy	1876	CAGACATGCCCCACAGTGCCTTCACAGCAGCGGGCCCTGCCACCACATCACCGGCCTGTGT	1935
Db	678	CAGACATGCCCCACAGTGCCTTCACAGCAGCGGGCCCTGCCACCACATCACCGGCCTGTGT	737
Qy	1936	GACTGCTTGCCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGTCCCAGTGGCAGATTT	1995
Db	738	GACTGCTTGCCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGTCCCAGTGGCAGATTT	797
Qy	1996	GGGAAAAAAGTGTGCAGGAATTTGTACCTGCACCAACAACGGAACCTGTAACCCCATTGAC	2055
Db	798	GGGAAAAAAGTGTGCAGGAATTTGTACCTGCACCAACAACGGAACCTGTAACCCCATTGAC	857
Qy	2056	AGATCTTGTGAGTGTACCCCGGTTGGATTGGCAGTGAAGTGTGTCCCAGTGGCAGATTT	2115
Db	858	AGATCTTGTGAGTGTACCCCGGTTGGATTGGCAGTGAAGTGTGTCCCAGTGGCAGATTT	917
Qy	2116	GCCCACTGGGGCCCAAAGTGCATCCACACGTGCAACTGCCATAATGGAGCTTTCTGCAGC	2175
Db	918	GCCCACTGGGGCCCAAAGTGCATCCACACGTGCAACTGCCATAATGGAGCTTTCTGCAGC	977
Qy	2176	GCCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTCTACTGCACTCAGAGA	2235
Db	978	GCCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTCTACTGCACTCAGAGA	1037
Qy	2236	TGTCCTCTAGGGTTTTATGGAAAAGATTGTGCACTGATATGCCAATGTCAAACGGAGCT	2295
Db	1038	TGTCCTCTAGGGTTTTATGGAAAAGATTGTGCACTGATATGCCAATGTCAAACGGAGCT	1097
Qy	2296	GACTGCGACCACATTTCTGGGCGAGTGTACTTGCCGCACTGGATTTCATGGGACGGGCACTGT	2355

Db 1098 GACTGCGACCACATTTCTGGGCAGTGTACTTGCCGCACTGGATTCATGGGACGGCACTGT 1157
 Qy 2356 GAGCAGAAGTGCCCTTCAGGAACATATGGCTATGGCTGTCGCCAGATATGTGATTGTCTG 2415
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1158 GAGCAGAAGTGCCCTTCAGGAACATATGGCTATGGCTGTCGCCAGATATGTGATTGTCTG 1217
 Qy 2416 AACAACTCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGCCCCGGATGGAAGGGA 2475
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1218 AACAACTCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGCCCCGGATGGAAGGGA 1277
 Qy 2476 GCGAGATGTGATCAAGCTGGTGTTCATAGTTGGAAATCTGAACAGCTTAAGCCGAACC 2535
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1278 GCGAGATGTGATCAAGCTGGTGTTCATAGTTGGAAATCTGAACAGCTTAAGCCGAACC 1337
 Qy 2536 AGTACTGCTCTCCCTGCTGATTCCTACCAGATCGGGGCCATTGCAGGCATCATCATTCTT 2595
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1338 AGTACTGCTCTCCCTGCTGATTCCTACCAAATCGGGGCCATTGCAGGCATCATCATTCTT 1397
 Qy 2596 GTCCTAGTTGTTCTCTTCCTACTGGCATTGTTTCATTATTTATAGACACA 2644
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1398 GTCCTAGTTGTTCTCTTCCTACTGGCATTGTTTCATTATTTATAGACACA 1446

RESULT 7

ABZ36212

ID ABZ36212 standard; cDNA; 1273 BP.

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AC ABZ36212;

XX

DT 10-FEB-2003 (first entry)

XX

DE Human secretory polynucleotide SPTM SEQ ID NO 376.

XX

KW Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia;

KW asthma; Crohn's disease; neurological disorder; epilepsy; cancer;

KW Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;

KW multiple sclerosis; Parkinson's disease; cell proliferative disorder;

KW anti-inflammatory; immunosuppressive; neuroprotective; nootropic;

KW neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic;

KW antipsoriatic; antianaemic; anti-HIV; human immunodeficiency virus;

KW secretory polynucleotide; secretory protein; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200283876-A2.

XX

PD 24-OCT-2002.

XX

PF 27-MAR-2002; 2002WO-US009921.

XX

PR 29-MAR-2001; 2001US-0280067P.

PR 29-MAR-2001; 2001US-0280068P.

PR 16-MAY-2001; 2001US-0291280P.

PR 17-MAY-2001; 2001US-0291829P.

PR 17-MAY-2001; 2001US-0291849P.

PR 19-JUN-2001; 2001US-0299428P.

PR 20-JUN-2001; 2001US-0299776P.

PR 20-JUN-2001; 2001US-0300001P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;

XX

DR WPI; 2003-075543/07.

DR P-PSDB; ABP75770.

XX

PT New human secretory proteins and polynucleotides, useful for diagnosing,
PT treating or preventing autoimmune/inflammatory disorders (e.g. AIDS),
PT neurological disorders (e.g. Alzheimer's), or cell proliferations or
PT cancers.

XX

PS Claim 1; SEQ ID NO 376; 458pp + Sequence Listing; English.

XX

CC The invention relates to a secretory polynucleotide (designated sptm)
CC comprising any of 567 polynucleotide sequences (ABZ35837-ABZ36403), a
CC naturally occurring polynucleotide sequence at least 90 % identical to
CC the polynucleotide sequence, a polynucleotide complementary to them or an
CC RNA equivalent of them. The polypeptide or polynucleotide are useful for
CC treating, preventing or diagnosing a disease or condition associated with
CC the expression of functional SPTM. These are particularly useful for
CC diagnosing, treating or preventing autoimmune/inflammatory disorders
CC (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's
CC disease), neurological disorders (e.g. epilepsy, Huntington's disease,
CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,
CC multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety,
CC schizophrenia or amnesia), or cell proliferative disorders (e.g.
CC psoriasis, polycythemia vera, or cancers including adenocarcinoma,
CC leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain,
CC breast, cervix or prostate). Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 1273 BP; 356 A; 311 C; 297 G; 309 T; 0 U; 0 Other;

Query Match 30.7%; Score 1049.4; DB 7; Length 1273;

Best Local Similarity 99.9%; Pred. No. 3.9e-294;

Matches 1050; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2373 AGGAACATATGGCTATGGCTGTGCGCCAGATATGTGATTGTCTGAACAACTCCACCTGCCA 2432

|||||

Db 1 AGGAACATATGGCTATGGCTGTGCGCCAGATATGTGATTGTCTGAACGACTCCACCTGCCA 60

Qy 2433 CCACATCACTGGGACCTGTTACTGCAGCCCCGGATGGAAGGGAGCGAGATGTGATCAAGC 2492

|||||

Db 61 CCACATCACTGGGACCTGTTACTGCAGCCCCGGATGGAAGGGAGCGAGATGTGATCAAGC 120

Qy 2493 TGGTGTTCATCATAGTTGGAAATCTGAACAGCTTAAGCCGAACCACTGCTCTCCCTGC 2552

|||||

Db 121 TGGTGTTCATCATAGTTGGAAATCTGAACAGCTTAAGCCGAACCACTGCTCTCCCTGC 180

Qy	2553	TGATTCTACCAGATCGGGGCCATTGCAGGCATCATCATTCTTGTCTAGTTGTTCTCTT	2612
Db	181	TGATTCTACCAGATCGGGGCCATTGCAGGCATCATCATTCTTGTCTAGTTGTTCTCTT	240
Qy	2613	CCTACTGGCATTGTTTCATTATTTATAGACACAAGCAGAAGGGAAAGGAATCAAGCATGCC	2672
Db	241	CCTACTGGCATTGTTTCATTATTTATAGACACAAGCAGAAGGGAAAGGAATCAAGCATGCC	300
Qy	2673	AGCAGTTACCTACACCCCTGCTATGAGGGTCGTCAATGCAGATTATACCATTTTCAGGAAC	2732
Db	301	AGCAGTTACCTACACCCCTGCTATGAGGGTCGTCAATGCAGATTATACCATTTTCAGGAAC	360
Qy	2733	CCTTCCTCACAGCAATGGTGGAAACGCTAATAGCCACTACTTCACCAATCCCAGTTACCA	2792
Db	361	CCTTCCTCACAGCAATGGTGGAAACGCTAATAGCCACTACTTCACCAATCCCAGTTACCA	420
Qy	2793	CACGCTCACCCAGTGTGCCACATCCCCTCACGTCAACAACAGGGACAGGATGACTGTCAC	2852
Db	421	CACGCTCACCCAGTGTGCCACATCCCCTCACGTCAACAACAGGGACAGGATGACTGTCAC	480
Qy	2853	GAAGTCAAAAAACAATCAACTGTTTGTGAATCTTAAAAATGTGAACCCTGGGAAGAGAGG	2912
Db	481	GAAGTCAAAAAACAATCAACTGTTTGTGAATCTTAAAAATGTGAACCCTGGGAAGAGAGG	540
Qy	2913	CCCTGTGGGGGACTGCAC'TGGGACATTGCCGGCTGACTGGAAACATGGCGGCTACCTCAA	2972
Db	541	CCCTGTGGGGGACTGCAC'TGGGACATTGCCGGCTGACTGGAAACATGGCGGCTACCTCAA	600
Qy	2973	CGAGCTCGGTGCTTTTGGACTTGACAGAAGCTATATGGGAAAATCCTTAAAAGACCTGGG	3032
Db	601	CGAGCTCGGTGCTTTTGGACTTGACAGAAGCTATATGGGAAAATCCTTAAAAGACCTGGG	660
Qy	3033	AAAGAATTCTGAATATAATTCAAGTAACTGCTCCCTAAGCAGTTCTGAGAACCCATATGC	3092
Db	661	AAAGAATTCTGAATATAATTCAAGTAACTGCTCCCTAAGCAGTTCTGAGAACCCATATGC	720
Qy	3093	CACTATTAAAGACCCACCTGTACTTATCCCGAAAAGCTCAGAGTGTGGTTATGTGGAGAT	3152
Db	721	CACTATTAAAGACCCACCTGTACTTATCCCGAAAAGCTCAGAGTGTGGTTATGTGGAGAT	780
Qy	3153	GAAATCGCCGGCACGAAGAGATTCCCACATATGCAGAGATCAATAACTCAACTTCAGCCAA	3212
Db	781	GAAATCGCCGGCACGAAGAGATTCCCACATATGCAGAGATCAATAACTCAACTTCAGCCAA	840
Qy	3213	CAGGAATGTCTATGAAGTTGAACCTACAGTGAGTGTGTCCAAGGAGTATTTCAGCAATAA	3272
Db	841	CAGGAATGTCTATGAAGTTGAACCTACAGTGAGTGTGTCCAAGGAGTATTTCAGCAATAA	900
Qy	3273	TGGGCGTCTCTCCCAGGATCCATATGACCTCCCAAAGAACAGTCACATCCCTTGTTCATTA	3332
Db	901	TGGGCGTCTCTCCCAGGATCCATATGACCTCCCAAAGAACAGTCACATCCCTTGTTCATTA	960
Qy	3333	TGACCTGCTGCCAGTCCGAGACAGTTCATCCTCCCCTAAGCAAGAGGACAGTGGAGGTAG	3392
Db	961	TGACCTGCTGCCAGTCCGAGACAGTTCATCCTCCCCTAAGCAAGAGGACAGTGGAGGTAG	1020
Qy	3393	CAGCAGCAACAGCAGCAGCAGCAGTGAATGA	3423

|||||
Db 1021 CAGCAGCAACAGCAGCAGCAGCAGTGAATGA 1051

RESULT 8

AAS91826

ID AAS91826 standard; cDNA; 1074 BP.

XX

AC AAS91826;

XX

DT 13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #27630.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX

DR WPI; 2001-639362/73.

DR P-PSDB; ABG27639.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX

PS Claim 1; SEQ ID NO 27630; 103pp; English.

XX

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 1074 BP; 241 A; 286 C; 303 G; 244 T; 0 U; 0 Other;

Query Match 18.1%; Score 618.4; DB 5; Length 1074;
Best Local Similarity 90.0%; Pred. No. 9.5e-169;
Matches 718; Conservative 0; Mismatches 1; Indels 79; Gaps 2;

```
Qy      412 GCCTGCGATGGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGG 471
          |||
Db      135 GCCTGCGATGGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGG 194

Qy      472 GCTCTGTGCAACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGC 531
          |||
Db      195 GCTCTGTGCAACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGC 254

Qy      532 TGCGAGGACCGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGC 591
          |||
Db      255 TGCGAGGACCGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGC 314

Qy      592 CAGAATGGAGCCACCTGCGACCACGTACGCGGGGAATGCCGCTGCCACCAGGATACACC 651
          |||
Db      315 CAGAATGGAGCCACCTGCGACCACGTACGCGGGGAATGCCGCTGCCACCAGGATACACC 374

Qy      652 GGAGCCTTCTGTGAGGATCTTTGTCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAGA 711
          |||
Db      375 GGAGCCTTCTGTGAGGATCTTTGTCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAGA 434

Qy      712 TGCCCTTGTCAAAAATGGAGGAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCT 771
          |||
Db      435 TGCCCTTGTCAAAAATGGAGGAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCT 494

Qy      772 GGCTGGAT----- 779
          |||
Db      495 GGCTGGATGTTGTCTTTCCCTGGCTGGAGGCCCATCTAATTTTCCAAGTCTCTTTGAATG 554

Qy      780 --GGGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAA 837
          |||
Db      555 CAGGGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAA 614

Qy      838 GAATGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGT 897
          |||
Db      615 GAATGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGT 674

Qy      898 CCAGGATACACAGGGGAAC-----GGTGCCAGGATGAGTG 932
          |||
Db      675 CCAGGATACACAGGGGAACGAGCAGCAGTTCCGGATGTTAGAAAGGTGCCAGGATGAGTG 734

Qy      933 TCCTGTTGGGACCTATGGCGTTCTCTGTGCTGAGACCTGCCAGTGTGTCAACGGAGGGAA 992
          |||
Db      735 TCCTGTTGGGACCTATGGCGTTCTCTGTGCTGAGACCTGCCAGTGTGTCAACGGAGGGAA 794
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QY 993 GTGTTACACGTGAGCGGCGCATGCCTCTGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGA 1052
 |||
 Db 795 GTGTTACACGTGAGCGGCGCATGCCTCTGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGA 854
 QY 1053 AGCACGCCTGTGTCCTGAGGGGCTCTACGGCATCAAATGTGACAAACGGTGTCCCTGCCA 1112
 |||
 Db 855 AGCACGCCTGTGTCCTGAGGGGCTCTACGGCATCAAATGTGACAAACGGTGTCCCTGCCA 914
 QY 1113 CTTGAAAACACTCATAG 1130
 |
 Db 915 CTTGAAAACACTCATAG 932

RESULT 9

AAF27791

ID AAF27791 standard; cDNA; 3567 BP.

XX

AC AAF27791;

XX

DT 05-APR-2001 (first entry)

XX

DE Rat TANGO 272 coding sequence SEQ ID NO: 19.

XX

KW Membrane associated protein; secreted protein; human; mouse; rat;

KW INTERCEPT 340; MANGO 003; MANGO 347; TANGO 272; TANGO 295; TANGO 354;

KW TANGO 378; skeletal disorder; cardiovascular disorder; renal disorder;

KW haematopoietic disorder; neural disorder; hepatic disorder;

KW neoplastic disease; ss.

XX

OS Rattus sp.

XX

PN WO200100673-A1.

XX

PD 04-JAN-2001.

XX

PF 29-JUN-2000; 2000WO-US018198.

XX

PR 30-JUN-1999; 99US-00345464.

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX

PI Barnes TM, Fraser CC, Wrighton N, Myers P, Busfield SJ, Sharp JD;

XX

DR WPI; 2001-050128/06.

DR P-PSDB; AAB66269.

XX

PT Isolated secreted or transmembrane proteins are used for diagnosis and

PT treatment of neoplastic and hematopoietic disorders e.g. T cell

PT disorders, cancer and tumors.

XX

PS Claim 1; Page 235-238; 294pp; English.

XX

CC The present invention provides the protein and coding sequences for a

CC number of membrane associated and secreted proteins from human, mouse and

CC rat. The proteins are designated INTERCEPT 340, MANGO 003, MANGO 347,

CC TANGO 272, TANGO 295, TANGO 254 and TANGO 378. The proteins are all

CC involved in signal transduction and the sequences can be used in the

CC treatment of cardiovascular, renal, hepatic, neural, neoplastic, skeletal
CC and haematopoietic disorders
XX
SQ Sequence 3567 BP; 690 A; 1115 C; 1000 G; 762 T; 0 U; 0 Other;

Query Match 17.8%; Score 608.4; DB 4; Length 3567;
Best Local Similarity 56.7%; Pred. No. 1.6e-165;
Matches 1226; Conservative 0; Mismatches 901; Indels 37; Gaps 4;

```
Qy      67 GCATCACCTCTGAATCTTGAAGACCCCTAATGTGTGTAGCCACTGGGAAAGCTACTCAGTG 126
      ||  | | || ||  | || | | || || | | || || || || || | | | |
Db      236 GCTGGAACACTCAACTCCAATGATCCCAATGTCTGTACCTTCTGGGAAAGCTTCACCACG 295

Qy      127 ACTGTGCAAGAGTCATACCCACATCCCTTT---GATCAAATTTACTACACGAGCTGCACT 183
      ||  | || || | || | | || ||  | | | | || ||
Db      296 ACCACTAAGGAGTCCCACCTTCGCCCCCTTCAGCCTGCCCCAGCCGAGTCCTGCGACAGG 355

Qy      184 GACATTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCTATCGA 243
      |  | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      356 CCCTGGGAAGACCCCCACACCTGCGCTCAGCCTACGGTTGTCTACCGGACTGTGTACCGT 415

Qy      244 CATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGT'TGTCCTGGATTTTATGAAAGC 303
      || | | || || | | | | | | | | | | | | | | | | | | | |
Db      416 CAGGTGGTGAAGATGGACTCCCGCCACGCCTGCAGTGCTGTGGGGGTTACTACGAGAGC 475

Qy      304 GGGGAAATGTGTGTCCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTGCTCCA 363
      | | | | || || || | || || | | | | || || || || || || ||
Db      476 AGTGGAGCCTGTGTCCCACTCTGTGCCAGGAGTGTGTCCACGGTCGCTGTGTGGCTCCT 535

Qy      364 AACACCTGTCTAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGATGGT 423
      ||  || || || || || || || || || | || || || || || || | |
Db      536 AATCGGTGCCAGTGTGCACCAGGCTGGCGGGGTGACGACTGTTCCAGTGAGTGTGCTCCT 595

Qy      424 GATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGCAAC 483
      |  || || || || || || || | || || || || || | | | | | |
Db      596 GGAATGTGGGGACCACAGTGTGACAGGCTCTGCCTCTGTGGCAACAGCAGTTCCTGTGAT 655

Qy      484 CCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGACCGC 543
      || || | || || || || | | | | | | | | | | || || | |
Db      656 CCCAGGAGTGGGGTGTGTTTTTGGCCCTCTGGCCTGCAGCCCCCGACTGCCTTCAGCCT 715

Qy      544 TGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATGGAGCC 603
      ||  | || | || || || | || || | || || || | || || ||
Db      716 TGCCCCGATGGCCACTATGGTCCTGCCTGCCAGTTTGATTGCCATTGC---TATGGGGCA 772

Qy      604 ACCTGCGACCACGTACGCGGGGAATGCCGCTGCCACCAGGATACACCGGAGCCTTCTGT 663
      || || || || | || | || | || || || || || || || || ||
Db      773 TCCTGTGACCCCCGGGATGGAGCCTGCTTCTGCCCCCAGGGAGAACAGGACCCAGGGCA 832

Qy      664 GAGGATCTTTGTCCTCCTGGTAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGTCAA 723
      |  || | || | || | | | | | | | | | | | | | | | |
Db      833 CTGATGGCTTCTTCTGCCCCAGAAC-----TTATCCTTGCCAA 870

Qy      724 AATGGAGGAGTGTGTATCACGTCACCTGAGAGTGTGCTCTTGCCCTTCTGGCTGGATGGGC 783
      || || || || || | || | || | || || || || || || || ||
Db      871 AATGGAGGTGTTCTCAGGGCTCTCAAGGCTCCTGCAGCTGCCCCACGGGGCTGGATGGGT 930
```

Qy	784	ACAGTGTGTGGTTCAGCCTTGCCCGAGGGTTCGCTTTGGAAAGAAGCTGTTCCCAAGAATGC	843
Db	931	GTTCATCTGTTCCCTGCCATGCCCAGAGGGTTTCCACGGACCCAAGTGTACTCAGGAATGT	990
Qy	844	CAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCAGGA	903
Db	991	CGTTGCCACAATGGTGGCCTTTGTGACAGGTTTACTGGGCAGTGCCACTGTGCTCCTGGC	1050
Qy	904	TACACAGGGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGTGCT	963
Db	1051	TATATCGGGGATCGGTGCCGTGAAGAGTGCCTGTGGGCCGCTTCGGTCAAGACTGTGCT	1110
Qy	964	GAGACCTGCCAGTGTGTCAACGGAGGGAAGTGTACCACGTGAGCGGCGCATGCCTCTGT	1023
Db	1111	GAGACCTGTGACTGTGCTCCTGGCGCTCGTTGCTTTCTGCCAATGGCGCGTGTCTGTGC	1170
Qy	1024	GAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCTGAGGGGCTCTACGGC	1083
Db	1171	GAACATGGCTTCACAGGCGACCGCTGCACTGAGCGACTCTGTCCAGATGGCCGCTATGGT	1230
Qy	1084	ATCAAATGTGACAAACGGTGTCCCTGCCACTTGGAACAACTCATAGCTGTACCCCATG	1143
Db	1231	CTGAGCTGCCAAGATCCCTGCACCTGCGACCCAGAACACAGTCTCAGCTGCCACCCAATG	1290
Qy	1144	TCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGTTCT	1203
Db	1291	CACGGCGAGTGTCTCCTGCCAGCCAGGTTGGGCGGGCCTCCACTGCAACGAGAGCTGCCCT	1350
Qy	1204	CCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGT	1263
Db	1351	CAGGACACGCACGGAGCCGGTTGCCAGGAGCACTGCCTCTGTCTGCACGGCGGTGTTTGC	1410
Qy	1264	GACAGTGTGACTGGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACC	1323
Db	1411	CTCGCCGACAGCGGCCTCTGCCGGTGTGCACCTGGCTACACGGGACCTCACTGCGCTAAT	1470
Qy	1324	CCATGCCCTCTGGGAACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAATGAT	1383
Db	1471	CTTTGTCCACCTAACACTTATGGGATCAACTGTTCTCCCACTGCTCCTGTGAAAATGCC	1530
Qy	1384	GCAGTCTGCTCTCCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCACGGGGTGGAC	1443
Db	1531	ATTGCTGTCTCTCCTGTGACGGCACGTGCATCTGCAAGGAAGGTTGGCAGCGTGGTAAC	1590
Qy	1444	TGCTCCATCAGATGTCCCAGTGGCACATGGGGCTTTGGCTGTAACCTAACATGCCAGTGC	1503
Db	1591	TGCTCTGTGCCCTGTCCCCCTGGCACCTGGGGCTTCAGTTGCAATGCCAGTTGCCAGTGT	1650
Qy	1504	CTCAACGGGGGAGCCTGCAACACCTGGACGGGACCTGCACGTGTGCACCTGGATGGCGC	1563
Db	1651	GCCCACGAGGGAGTCTGCAGCCCCAACTGGAGCCTGTACTTGACCCCTGGGTGGCGT	1710
Qy	1564	GGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAGCGC	1623
Db	1711	GGGGTTCACTGCCAACTTCCGTGCCCGAAGGGACAGTTTGGTGAAGGTTGTGCCAGTGT	1770
Qy	1624	TGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTCCCG	1683

KW Parkinson's disease; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 243. .3227
 FT /*tag= a
 FT /product= "CADHP-6"
 XX
 PN WO200259312-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 18-DEC-2001; 2001WO-US049206.
 XX
 PR 18-DEC-2000; 2000US-0256542P.
 PR 22-DEC-2000; 2000US-0259604P.
 PR 05-JAN-2001; 2001US-0260101P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Duggan BM, Xu Y, Lee EA, Lee S, Lu DAM, Warren BA, Yue H;
 PI Gietzen KJ, Honchell CD, Burford N, Baughn MR, Tang TY, Hillman JL;
 PI Gandhi AR, Kallick DA, Bandman O, Graul RC, Walia NK, Lu Y;
 PI Ramkumar J, Yao MG, Lal PG;
 XX
 DR WPI; 2002-590826/63.
 DR P-PSDB; AAG79417.
 XX
 PT New human cell adhesion proteins (CADHP) useful for treating, diagnosing
 PT and preventing diseases or conditions associated with the aberrant CADPH
 PT expression e.g. cancer, acquired immunodeficiency syndrome, Alzheimer's
 PT disease and epilepsy.
 XX
 PS Claim 5; Page 141-42; 149pp; English.
 XX
 CC The sequences given in ABA00054-63 encode novel human cell adhesion
 CC proteins (CADHP). The CADHP polypeptides and polynucleotides are useful
 CC in treating, diagnosing and preventing diseases or conditions associated
 CC with the decreased expression or overexpression of CADHP, e.g. immune
 CC system (acquired immunodeficiency syndrome, thymic dysplasia),
 CC neurological (Alzheimer's disease, Parkinson's disease, epilepsy),
 CC developmental (renal tubular acidosis, congenital glaucoma) and cell
 CC proliferative (cancer, atherosclerosis) disorders. They are also useful
 CC in assessing the effects of exogenous compounds on the expression of
 CC nucleic acid and amino acid sequences of CADHP. The CADHP or its
 CC fragments are useful in screening compounds for effectiveness as agonist
 CC or antagonist of the polypeptides, or in altering the expression of the
 CC target polynucleotide and compounds that specifically bind to or modulate
 CC the activity of the polypeptide. The protein encoded by this cDNA
 CC sequence shows homology to rat MEGF6
 XX
 SQ Sequence 3574 BP; 626 A; 1218 C; 1045 G; 685 T; 0 U; 0 Other;

Query Match 17.5%; Score 600.6; DB 6; Length 3574;
 Best Local Similarity 57.4%; Pred. No. 2.9e-163;
 Matches 1165; Conservative 0; Mismatches 849; Indels 15; Gaps 4;

Qy	62	GGACAGCATCACCTCTGAATCTTGAAGACCCTAATGTGTGTA GCCACTGGGAAAGCTACT	121
Db	289	GGCTGGCTGGA ACTCTCAACCC CAGTGATCCCA ATACCTGCAGCTTCTGGGAAAGCTTCA	348
Qy	122	CAGTGACTGTGCAAGAGTCATA CCCACATCCCTTTGATCAAATTTACTACACGAGCTGC-	180
Db	349	CTACCACCACCAAGGAGTCCC ACTCCCGCCCCCTTCAGCCTGCTCCCCTCAGAGCCCTGCG	408
Qy	181	--ACTGACATTCTAAACTGGTTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCT	238
Db	409	AGCGGCCCTGGGAGGGCCCCCATACTTGCCCCAGCCCACGGTTGTATACCGGACCGTGT	468
Qy	239	ATCGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTGTCCTGGATTTTATG	298
Db	469	ACCGTCAGGTGGTGAAGACGGACCACCGCCAGCGCCTGCAGTGCTGCCATGGCTTCTATG	528
Qy	299	AAAGCGGGGAAATGTGTGTCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTG	358
Db	529	AGAGCAGGGGGTTCTGTGTCCCGCTCTGTGCCAGGAGTGTGTCCATGGCCGTTGTGTGG	588
Qy	359	CTCCAAACACCTGT CAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCG	418
Db	589	CACCCAATCAGTGCCAATGTGTGCCAGGCTGGCGGGGCGACGACTGTTCCAGTGAGTGTG	648
Qy	419	ATGGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGT	478
Db	649	CCCCAGGAATGTGGGGGCCACAGTGTGACAAGCCCTGCAGCTGCGGCAACAACAGCTCGT	708
Qy	479	GCAACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGG	538
Db	709	GTGATCCCAAGAGTGGGGTATGTTCTTGCCCTTCTGGTCTGCAGCCCCGAACTGCCTTC	768
Qy	539	ACCGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATG	598
Db	769	AGCCCTGTACCCCTGGCTACTATGGCCCTGCCTGCCAGTTC CGCTGCCAGTGCC--ATG	825
Qy	599	GAGCCACCTGCGACCACGTACG GGGGAATGCCGCTGCCCACCAGGATACACCGGAGCCT	658
Db	826	GGGCACCCTGCGATCCCCAGACTGGAGCCTGCTTCTGCCCCGAGAGAGAACTGGGCCCCA	885
Qy	659	TCTGTGAGGATCTTTGTCCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTT	718
Db	886	GCTGTGACGTGTCCTGTTCCAGGGCAC TTTCTGGCTTCTTCTGCCCCAGCACCCATCCTT	945
Qy	719	GTCAAAATGGAGGAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGA	778
Db	946	GCCAAAATGGAGGTGTCTTCCAAACCCACAGGGCTCCTGCAGCTGCCCCCTGGCTGGA	1005
Qy	779	TGGGCACAGTGTGTGGTCAGCCTTGCCCCAGGGTCGCTTTGGAAAGAACTGTTCCCAAG	838
Db	1006	TGGGCACCATCTGCTCCCTGCCCTGCCAGAGGGCTTTCACGGACCCA CTGCTCCCAGG	1065
Qy	839	AATGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTC	898
Db	1066	AATGTCGCTGCCACAACGGCGGCCTCTGTGACCGATTCACTGGGCAGTGCCGCTGCGCTC	1125

Qy	899	CAGGATACACAGGGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCT	958
Db	1126	CGGGTTACACTGGGGATCGGTGCCGGGAGGAGTGCCCGGTGGGCCGCTTTGGGCAGGACT	1185
Qy	959	GTGCTGAGACCTGCCAGTGTGTCAACGGAGGGAAGTGTACCACGTGAGCGGCGCATGCC	1018
Db	1186	GTGCTGAGACGTGCGACTGCGCCCCGGACGCCCCTTGCTTCCCGGCCAACGGCGCATGTC	1245
Qy	1019	TCTGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCTTGAGGGGCTCT	1078
Db	1246	TGTGCGAACACGGCTTCACTGGGGACCGCTGCACGGATCGCCTCTGCCCCGACGGCTTCT	1305
Qy	1079	ACGGCATCAAATGTGACAAACGGTGTCCCTGCCACTTGAAAAACATCATAGCTGTCACC	1138
Db	1306	ACGGTCTCAGCTGCCAGGCCCTTGCACCTGCGACCGGGAGCACAGCCTCAGCTGCCACC	1365
Qy	1139	CCATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACAT	1198
Db	1366	CGATGAACGGGGAGTGTCTCTGCCTGCCGGGCTGGGCGGGCCTCCACTGCAACGAGAGCT	1425
Qy	1199	GTTCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAG	1258
Db	1426	GCCCGCAGGACACGCATGGGCCAGGGTGCCAGGAGCACTGTCTCTGCCTGCACGGTGGCG	1485
Qy	1259	ACTGTGACAGTGTGACTGGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCT	1318
Db	1486	TCTGCCAGGCTACCAGCGGCCTCTGTCACTGCGCGCCGGGTTACACGGGGCCCTCACTGTG	1545
Qy	1319	CTACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAA	1378
Db	1546	CTAGTCTTTGTCTCCTGACACCTACGGTGTCAACTGTTCTGCACGCTGCTCATGTGAAA	1605
Qy	1379	ATGATGCAGTCTGCTCTCCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCACGGGG	1438
Db	1606	ATGCCATCGCCTGCTCACCCATCGACGGCGAGTGCCTCTGCAAGGAAGGTTGGCAGCGTG	1665
Qy	1439	TGGACTGCTCCATCAGATGTCCCAGTGGCACATGGGGCTTTGGCTGTAACCTAACATGCC	1498
Db	1666	GTAAGTGTCTGTGCCCTGCCACCCGGAACCTGGGGCTTCAGTTGCAATGCCAGCTGCC	1725
Qy	1499	AGTGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGAT	1558
Db	1726	AGTGTGCCCATGAGGCAGTCTGCAGCCCCCAAACCTGGAGCCTGTACCTGCACCCCTGGGT	1785
Qy	1559	GGCGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTG	1618
Db	1786	GGCATGGGGCCCACTGCCAGCTGCCCTGTCCGAAGGGGCAGTTTGAGAAAGGTTGTGCCA	1845
Qy	1619	AGCGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCC	1678
Db	1846	GTCGCTGTGACTGTGACCACTCTGATGGCTGTGACCCTGTTTCATGGACGCTGTCAGTGCC	1905
Qy	1679	TCCCGGGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCA	1738
Db	1906	AGGCTGGCTGGATGGGTGCCCGCTGCCACCTGTCTCTGCCCTGAGGGCTTATGGGGAGTCA	1965
Qy	1739	ACTGCTCCCTGCCCTGCTACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCT	1798

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      |||| | |||| ||| || ||||| | || ||||| ||||| ||
Db      1966 ACTGTAGCAACACCTGCACCTGCAAGAATGGGGGCACCTGTCTCCCTGAGAATGGCAACT 2025

Qy      1799 GCGAGTGTGCACCAGGCTTCCGAGGCACCACTTGTCTCAGAGGATCTGCTCCCCTGGTTTTT 1858
      ||| ||||| || |||| ||| || | || |||| ||| |||| |
Db      2026 GCGTGTGTGCACCCGGATTCCGGGGCCCCCTCCTGCCAGAGATCCTGTCTCAGCCTGGCCGCT 2085

Qy      1859 ATGGGCATCGCTGCAGCCAGACATGCCCACAGTGCCTTCACAGCAGCGGGCCCTGCCACC 1918
      |||| | |||| | | | |||| | || | | |||||
Db      2086 ATGGCAAACGCTGTGTGC-----CCTGCAAGTGCCTAACCACTCC---TTCTGCCACC 2136

Qy      1919 ACATCACCGGCCTGTGTGACTGCTTGCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGT 1978
      | | ||| || |||| || ||||| ||||| || |||| | |
Db      2137 CCTCGAACGGGACCTGCTACTGCCTGGCTGGCTGGACAGGCCCCGACTGCTCCCAGCGCT 2196

Qy      1979 GTCCCAGTGGCAGATTTGGGAAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAA 2038
      | || || | |||| | |||| | | || || | ||
Db      2197 GCCCTCTGGGGACATTTGGTGCTAACTGCTCCCAGCCATGCCAGTGTGGTCCTGGAGAAA 2256

Qy      2039 CCTGTAACCCATTGACAGATCTTGTCTAGTGTACCCCGGTTGGATTGG 2087
      || |||| | | ||| ||| ||| || | |||
Db      2257 AGTGCCACCCAGAGACTGGGGCCTGTGTATGTCCCCCAGGGCACAGTGG 2305

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RESULT 11

AAS86746

ID AAS86746 standard; cDNA; 1402 BP.

XX

AC AAS86746;

XX

DT 13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #22550.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX

DR WPI; 2001-639362/73.

DR P-PSDB; ABG22559.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX

PS Claim 1; SEQ ID NO 22550; 103pp; English.

XX

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 1402 BP; 356 A; 335 C; 413 G; 298 T; 0 U; 0 Other;

Query Match 17.0%; Score 581.6; DB 5; Length 1402;
Best Local Similarity 88.5%; Pred. No. 5.7e-158;
Matches 710; Conservative 0; Mismatches 9; Indels 83; Gaps 4;

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Qy      412 GCCTGCGATGGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGG 471
      |||
Db      135 GCCTGCGATGGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGG 194

Qy      472 GCTCTGTGCAA-CCCCATCACCGGGGCTTGC---CACTGTGCTGCGGGCTTCCGGGGCTG 527
      |||
Db      195 GCTCTGTGCAACCCCCATCACCGGGGCTTGCCACTGTGGCTGCGGGGCTTCCGGGGCTG 254

Qy      528 GCGCTGCGAGGACCGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCA 587
      |||
Db      255 GCGCTGCGAGGACCGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCA 314

Qy      588 GTGCCAGAATGGAGCCACCTGCGACCACGTACGGGGGAATGCCGCTGCCACCAGGATA 647
      |||
Db      315 GTGCCAGAATGGAGCCACCTGCGACCACGTACGGGGGAATGCCGCTGCCACCAGGATA 374

Qy      648 CACCGGAGCCTTCTGTGAGGATCTTTGTCCTCCTGGTAAACATGGTCCACAGTGTGAGCA 707
      |||
Db      375 CACCGGAGCCTTCTGTGAGGATCTTTGTCCTCCTGGTAAACATGGTCCACAGTGTGAGCA 434

Qy      708 GAGATGCCCTTGTCAAAATGGAGGAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCC 767
      |||
Db      435 GAGATGCCCTTGTCAAAATGGAGGAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCC 494
```

Qy	768	TTCTGGCTGGAT-----	779
Db	495	TTCTGGCTGGATGTTGTCTTCCCTGGCTGGAGGCCCATCTAATTTTCCAAGTCTCTTTG	554
Qy	780	-----GGGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTC	833
Db	555	AATGCAGGGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTC	614
Qy	834	CCAAGAATGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTG	893
Db	615	CCAAGAATGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTG	674
Qy	894	CAGTCCAGGATACACAGGGGAAC-----GGTGCCAGGATG	928
Db	675	CAGTCCAGGATACACAGGGGAACGAGCAGCAGTTCCGGATGTTAGAAAGGTGCCAGGATG	734
Qy	929	AGTGTCTCTGTTGGGACCTATGGCGTTCTCTGTGCTGAGACCTGCCAGTGTGTCAACGGAG	988
Db	735	AGTGTCTCTGTTGGGACCTATGGCGTTCTCTGTGCTGAGACCTGCCAGTGTGTCAACGGAG	794
Qy	989	GGAAGTGTTACCACGTGAGCGGCGCATGCCTCTGTGAAGCAGGCTTTGCTGGCGAGCGCT	1048
Db	795	GGAAGTGTTACCACGTGAGCGGCGCATGCCTCTGTGAAGCAGGCTTTGCTGGCGAGCGCT	854
Qy	1049	GCGAAGCACGCCTGTGTCTCTGAGGGGCTCTACGGCATCAAATGTGACAAACGGTGTCCCT	1108
Db	855	GCGAAGCACGCCTGTGTCTCTGAGGGGCTCTACGGCATCAAATGTGACAAACGGTGTCCCT	914
Qy	1109	GCCACTTGAAAAACACTCATAG	1130
Db	915	GCCACCTTGAAAAACACTCATAG	936

RESULT 12

AAS72218

ID AAS72218 standard; cDNA; 936 BP.

XX

AC AAS72218;

XX

DT 13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #8022.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX

PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR P-PSDB; ABG08031.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 1; SEQ ID NO 8022; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 936 BP; 200 A; 239 C; 258 G; 239 T; 0 U; 0 Other;

Query Match 16.5%; Score 563.8; DB 5; Length 936;
 Best Local Similarity 97.9%; Pred. No. 6.8e-153;
 Matches 571; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1130 GCTGTCACCCCATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTA 1189
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 95 GCTGTCACCCCATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTA 154
 Qy 1190 ATGAGACATGTTCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAA 1249
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 155 ATGAGACATGTTCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAA 214
 Qy 1250 ATGGGGCAGACTGTGACAGTGTGACTGGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAA 1309
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 215 ATGGGGCAGACTGTGACAGTGTGACTGGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAA 274
 Qy 1310 TTGACTGCTCTACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTTCCTCTCGTGTG 1369
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 275 TTGACTGCTCTACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTTCCTCTCGTGTG 334

QY 1370 GCTGTAAAAATGATGCAGTCTGCTCTCCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCT 1429
 |||
 Db 335 GCTGTAAAAATGATGCAGTCTGCTCTCCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCT 394
 QY 1430 GGCACGGGGTGGACTGCTCCATCAGATGTCCCAGTGGCACATGGGGCTTTGGCTGTAACT 1489
 |||
 Db 395 GGCACGGGGTGGACTGCTCCATCAGATGTCCCAGTGGCACATGGGGCTTTGGCTGTAACT 454
 QY 1490 TAACATGCCAGTGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTG 1549
 |||
 Db 455 TAACATGCCAGTGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTG 514
 QY 1550 CACCTGGATGGCGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGA 1609
 |||
 Db 515 CACCTGGATGGCGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGA 574
 QY 1610 ACTGTGCTGAGCGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGGCCATT 1669
 |||
 Db 575 ACTGTGCTGAGCGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGGCCATT 634
 QY 1670 GCCGCTGCCTCCCGGGATGGTCAGGTGTCCACTGTGACAGCGT 1712
 |||
 Db 635 GCCGCTGCCTCCCGGGATGGTCAGGTGTCCACTGTGACAGCGT 677

RESULT 13

ACD05889

ID ACD05889 standard; cDNA; 936 BP.

XX

AC ACD05889;

XX

DT 06-AUG-2003 (first entry)

XX

DE Novel human contig #63.

XX

KW Human; angiogenesis; cytokine; cell proliferation; pluripotent;
 KW cell differentiation; totipotent; stem cell; transplantation; bio-sensor;
 KW neuroepithelial cell; autoimmune disease; neural cell; genetic disorder;
 KW nerve; brain tissue; central nervous system disease;
 KW peripheral nervous system disease; neuropathy; haematopoiesis; bone;
 KW myeloid disorder; lymphoid cell disorder; platelet disorder; tendon;
 KW regeneration; cartilage; tendon; ligament; nerve tissue growth;
 KW tissue repair; wound healing; burn; ulcer; osteoporosis; cancer;
 KW osteoarthritis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung fibrosis; liver fibrosis; reperfusion injury;
 KW immune deficiency; infection; autoimmune disorder; allergic reaction;
 KW thrombolysis; thrombosis; coagulation disorder; hereditary disorder;
 KW biorhythm; circadian cycle; fertility; metabolism; catabolism; anabolism;
 KW nootropic; neuroprotective; antiparkinsonian; anticonvulsant;
 KW haemostatic; vulnerary; antiulcer; osteopathic; antiarthritic;
 KW vasotropic; immunostimulant; antibacterial; fungicide; immunosuppressive;
 KW antirheumatic; antidiabetic; antiasthmatic; cytostatic; virucide;
 KW expressed sequence tag; EST; ss.

XX

OS Homo sapiens.

XX

PN WO2003023013-A2.
 XX
 PD 20-MAR-2003.
 XX
 PF 13-SEP-2002; 2002WO-US029001.
 XX
 PR 13-SEP-2001; 2001US-0322511P.
 PR 12-SEP-2002; 2002US-00243552.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Yang Y, Wang Z, Weng G, Ma Y;
 XX
 DR WPI; 2003-313249/30.
 DR P-PSDB; ABO00812.
 XX
 PT Novel nucleic acids and polypeptides for diagnosis, treatment of central
 PT and peripheral nervous system diseases and neuropathies, such as
 PT Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 PT lateral sclerosis.
 XX
 PS Example 2; SEQ ID NO 735; 300pp; English.
 XX
 CC The present invention relates to the isolation of novel human
 CC polynucleotide sequences and their encoding polypeptides. The novel
 CC polypeptides exhibit activities relating to angiogenesis, cytokine, cell
 CC proliferation, cell differentiation, antiinflammatory, and stem cell
 CC growth factor activities. The polypeptides are involved in the
 CC proliferation, differentiation and survival of pluripotent and totipotent
 CC stem cells, and are useful for re-engineering damaged or diseased
 CC tissues, transplantation, manufacture of bio-pharmaceuticals and
 CC development of bio-sensors. The polypeptides can be used to manipulate
 CC stem cells in culture to give rise to neuroepithelial cells that can be
 CC used to augment or replace cells damaged by illness, autoimmune disease,
 CC accidental damage or genetic disorders. The polypeptides induce the
 CC proliferation of neural cells and regeneration of nerve and brain tissue
 CC and are useful for the treatment of central and peripheral nervous system
 CC diseases and neuropathies, such as Alzheimer's, Parkinson's disease,
 CC Huntington's disease, amyotrophic lateral sclerosis (ALS). The
 CC polypeptides are also involved in chemotactic or chemokinetic activity,
 CC regulation of haematopoiesis and are useful for treating myeloid or
 CC lymphoid cell disorders, platelet disorders such as thrombocytopaenia and
 CC for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
 CC growth, in tissue repair, healing of burns, incisions, ulcers, for
 CC treating osteoporosis, osteoarthritis, bone degenerative disorders, and
 CC periodontal disease. The polypeptides are also useful for gut protection
 CC or regeneration and treatment of lung or liver fibrosis, reperfusion
 CC injury in various tissues, various immune deficiencies and disorders
 CC including severe combined immunodeficiency (SCID), bacterial or fungal
 CC infections, autoimmune disorders (e.g. multiple sclerosis, rheumatoid
 CC arthritis, diabetes mellitus, myasthenia gravis), allergic reactions and
 CC conditions, such as asthma or other respiratory problems. The
 CC polypeptides are involved in thrombolysis or thrombosis and are useful in
 CC treatment of various coagulation disorders (including hereditary
 CC disorders such as haemophilia) or to enhance coagulation and other
 CC haemostatic events in treating wounds resulting from trauma, surgery or
 CC other causes. The polypeptides exhibit immune stimulating or immune

RESULT 14

ACD05589

ID ACD05589 standard; cDNA; 936 BP.

XX

AC ACD05589;

XX

DT 06-AUG-2003 (first entry)

XX

DE cDNA encoding novel human polypeptide #99.

XX

KW Human; angiogenesis; cytokine; cell proliferation; pluripotent;
 KW cell differentiation; totipotent; stem cell; transplantation; bio-sensor;
 KW neuroepithelial cell; autoimmune disease; neural cell; genetic disorder;
 KW nerve; brain tissue; central nervous system disease;
 KW peripheral nervous system disease; neuropathy; haematopoiesis; bone;
 KW myeloid disorder; lymphoid cell disorder; platelet disorder; tendon;
 KW regeneration; cartilage; tendon; ligament; nerve tissue growth;
 KW tissue repair; wound healing; burn; ulcer; osteoporosis; cancer;
 KW osteoarthritis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung fibrosis; liver fibrosis; reperfusion injury;
 KW immune deficiency; infection; autoimmune disorder; allergic reaction;
 KW thrombolysis; thrombosis; coagulation disorder; hereditary disorder;
 KW biorhythm; circadian cycle; fertility; metabolism; catabolism; anabolism;
 KW nootropic; neuroprotective; antiparkinsonian; anticonvulsant;
 KW haemostatic; vulnerary; antiulcer; osteopathic; antiarthritic;
 KW vasotropic; immunostimulant; antibacterial; fungicide; immunosuppressive;
 KW antirheumatic; antidiabetic; antiasthmatic; cytostatic; virucide; gene;
 KW ss.

XX

OS Homo sapiens.

XX

PN WO2003023013-A2.

XX

PD 20-MAR-2003.

XX

PF 13-SEP-2002; 2002WO-US029001.

XX

PR 13-SEP-2001; 2001US-0322511P.

PR 12-SEP-2002; 2002US-00243552.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Yang Y, Wang Z, Weng G, Ma Y;

XX

DR WPI; 2003-313249/30.

DR P-PSDB; ABO00512.

XX

PT Novel nucleic acids and polypeptides for diagnosis, treatment of central
 PT and peripheral nervous system diseases and neuropathies, such as
 PT Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 PT lateral sclerosis.

XX

PS Claim 1; SEQ ID NO 99; 300pp; English.

XX

CC The present invention relates to the isolation of novel human
 CC polynucleotide sequences and their encoding polypeptides. The novel
 CC polypeptides exhibit activities relating to angiogenesis, cytokine, cell

CC proliferation, cell differentiation, antiinflammatory, and stem cell
CC growth factor activities. The polypeptides are involved in the
CC proliferation, differentiation and survival of pluripotent and totipotent
CC stem cells, and are useful for re-engineering damaged or diseased
CC tissues, transplantation, manufacture of bio-pharmaceuticals and
CC development of bio-sensors. The polypeptides can be used to manipulate
CC stem cells in culture to give rise to neuroepithelial cells that can be
CC used to augment or replace cells damaged by illness, autoimmune disease,
CC accidental damage or genetic disorders. The polypeptides induce the
CC proliferation of neural cells and regeneration of nerve and brain tissue
CC and are useful for the treatment of central and peripheral nervous system
CC diseases and neuropathies, such as Alzheimer's, Parkinson's disease,
CC Huntington's disease, amyotrophic lateral sclerosis (ALS). The
CC polypeptides are also involved in chemotactic or chemokinetic activity,
CC regulation of haematopoiesis and are useful for treating myeloid or
CC lymphoid cell disorders, platelet disorders such as thrombocytopaenia and
CC for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
CC growth, in tissue repair, healing of burns, incisions, ulcers, for
CC treating osteoporosis, osteoarthritis, bone degenerative disorders, and
CC periodontal disease. The polypeptides are also useful for gut protection
CC or regeneration and treatment of lung or liver fibrosis, reperfusion
CC injury in various tissues, various immune deficiencies and disorders
CC including severe combined immunodeficiency (SCID), bacterial or fungal
CC infections, autoimmune disorders (e.g. multiple sclerosis, rheumatoid
CC arthritis, diabetes mellitus, myasthenia gravis), allergic reactions and
CC conditions, such as asthma or other respiratory problems. The
CC polypeptides are involved in thrombolysis or thrombosis and are useful in
CC treatment of various coagulation disorders (including hereditary
CC disorders such as haemophilia) or to enhance coagulation and other
CC haemostatic events in treating wounds resulting from trauma, surgery or
CC other causes. The polypeptides exhibit immune stimulating or immune
CC suppressing activity, and are useful for treating autoimmune diseases or
CC cancer. They also inhibit the growth, infection or function of infectious
CC agents such as bacteria, fungi, viruses, effect biorhythms or circadian
CC cycles of rhythms, fertility of male or female subjects, metabolism,
CC catabolism, and anabolism. ACD05491-ACD05826 represent the novel cDNA
CC sequences of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 936 BP; 200 A; 239 C; 258 G; 239 T; 0 U; 0 Other;

Query Match 16.5%; Score 563.8; DB 7; Length 936;
Best Local Similarity 97.9%; Pred. No. 6.8e-153;
Matches 571; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1130 GCTGTCACCCCATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTA 1189
|
Db 95 GCTGTCACCCCATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTA 154

Qy 1190 ATGAGACATGTTCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAA 1249
|
Db 155 ATGAGACATGTTCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAA 214

Qy 1250 ATGGGGCAGACTGTGACAGTGTGACTGGAAAAGTGACACCTGTGCCCCAGGATTCAAAGGAA 1309
|

Db 215 ATGGGGCAGACTGTGACAGTGTGACTGGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAA 274

Qy 1310 TTGACTGCTCTACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCTCTCGCTGTG 1369
 |||

Db 275 TTGACTGCTCTACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCTCTCGCTGTG 334

Qy 1370 GCTGTAAAAATGATGCAGTCTGCTCTCCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCT 1429
 |||

Db 335 GCTGTAAAAATGATGCAGTCTGCTCTCCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCT 394

Qy 1430 GGCACGGGGTGGACTGCTCCATCAGATGTCCCAGTGGCACATGGGGCTTTGGCTGTAACT 1489
 |||

Db 395 GGCACGGGGTGGACTGCTCCATCAGATGTCCCAGTGGCACATGGGGCTTTGGCTGTAACT 454

Qy 1490 TAACATGCCAGTGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTG 1549
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Db 455 TAACATGCCAGTGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTG 514

Qy 1550 CACCTGGATGGCGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGA 1609
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Db 515 CACCTGGATGGCGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGA 574

Qy 1610 ACTGTGCTGAGCGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATT 1669
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Db 575 ACTGTGCTGAGCGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATT 634

Qy 1670 GCCGCTGCCTCCCCGGATGGTCAGGTGTCCACTGTGACAGCGT 1712
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Db 635 GCCGCTGCCTCCCCGGATGGTCAGTGTTCACCGGAAATGGTGT 677

RESULT 15

AAS72219

ID AAS72219 standard; cDNA; 2295 BP.

XX

AC AAS72219;

XX

DT 13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #8023.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

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OS Homo sapiens.

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PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR P-PSDB; ABG08032.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 1; SEQ ID NO 8023; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 2295 BP; 610 A; 543 C; 602 G; 540 T; 0 U; 0 Other;

Query Match 16.2%; Score 554; DB 5; Length 2295;
 Best Local Similarity 97.3%; Pred. No. 8.2e-150;
 Matches 574; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

Qy 2834 GGGACAGGATGACTGTCACGAAGTCAAAAAACAATCAACTGTTTGTGAATCTTAAAAATG 2893
 |||| | ||| | |||||
 Db 575 GGGAGGGACCAACTGCTCCAGTGTCAAAAAACAATCAACTGTTTGTGAATCTTAAAAATG 634

 Qy 2894 TGAACCCTGGGAAGAGAGGCCCTGTGGGGGACTGCACTGGGACATTGCCGGCTGACTGGA 2953
 |||||
 Db 635 TGAACCCTGGGAAGAGAGGCCCTGTGGGGGACTGCACTGGGACATTGCCGGCTGACTGGA 694

 Qy 2954 AACATGGCGGCTACCTCAACGAGCTCGGTGCTTTTGGACTTGACAGAAGCTATATGGGAA 3013
 |||||
 Db 695 AACATGGCGGCTACCTCAACGAGCTCGGTGCTTTTGGACTTGACAGAAGCTATATGGGAA 754

 Qy 3014 AATCCTTAAAAGACCTGGGAAAGAATTCTGAATATAATTCAAGTAAGTCTCCCTAAGCA 3073
 |||||
 Db 755 AATCCTTAAAAGACCTGGGAAAGAATTCTGAATATAATTCAAGTAAGTCTCCCTAAGCA 814

 Qy 3074 GTTCTGAGAACCCATATGCCACTATTAAAGACCCACCTGTACTTATCCCGAAAAGCTCAG 3133

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      |||
Db      815 GTTCTGAGAACCCATATGCCACTATTAAAGACCCACCTGTACTTATCCCGAAAAGCTCAG 874
Qy      3134 AGTGTGGTTATGTGGAGATGAAATCGCCGGCACGAAGAGATTCCCCATATGCAGAGATCA 3193
      |||
Db      875 AGTGTGGTTATGTGGAGATGAAATCGCCGGCACGAAGAGATTCCCCATATGCAGAGATCA 934
Qy      3194 ATAACTCAACTTCAGCCAACAGGAATGTCTATGAAGTTGAACCTACAGTGAGTGTGTCC 3253
      |||
Db      935 ATAACTCAACTTCAGCCAACAGGAATGTCTATGAAGTTGAACCTACAGTGAGTGTGTCC 994
Qy      3254 AAGGAGTATTCAGCAATAATGGGCGTCTCTCCAGGATCCATATGACCTCCCAAAGAACA 3313
      |||
Db      995 AAGGAGTATTCAGCAATAATGGGCGTCTTTCCAGGATCCATATGACCTCCC-AAGAACA 1053
Qy      3314 GTCACATCCCTTGTCAATTATGACCTGCTGCCAGTCCGAGACAGTTCATCCTCCCTAAGC 3373
      |||
Db      1054 GTCACATCCCTTGTCAATTATGACCTGCTGCCAGTCCGAGACAGTTCATCCTCCCTTAAGC 1113
Qy      3374 AAGAGGACAGTGGAGGTAGCAGCAGCAACAGCAGCAGCAGCAGTGAATGA 3423
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Db      1114 AAGAGGACAGTGGTGGTAGCAGCAGCAACAGCAGCAGCAGCAGTGAATGA 1163

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Job time : 1291 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 30, 2004, 02:09:56 ; Search time 235 Seconds
(without alignments)
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Perfect score: 3423
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	524.6	15.3	5197	4	US-09-833-381-1910
	3	165.8	4.8	1578	4	US-09-130-491-10
	4	156	4.6	1464	3	US-09-188-930-255
	5	156	4.6	1464	4	US-09-312-283C-255
	6	156	4.6	1635	4	US-09-312-283C-73
	7	155.2	4.5	1633	3	US-09-188-930-73
	8	134.4	3.9	393	4	US-09-833-381-1076
	9	66.2	1.9	553	4	US-09-621-976-1192
	10	55.2	1.6	4138	1	US-08-323-474-1
	11	55.2	1.6	4138	5	PCT-US93-06093-1

12	54	1.6	3845	2	US-08-220-240A-4	Sequence 4, Appli
13	54	1.6	4175	1	US-07-934-393B-1	Sequence 1, Appli
14	54	1.6	4175	1	US-08-278-089A-1	Sequence 1, Appli
15	54	1.6	4175	2	US-08-838-957A-1	Sequence 1, Appli
16	54	1.6	4176	1	US-08-278-089A-5	Sequence 5, Appli
17	54	1.6	4176	2	US-08-838-957A-5	Sequence 5, Appli
c 18	49	1.4	3489	2	US-08-728-323A-1	Sequence 1, Appli
c 19	49	1.4	3489	4	US-09-298-568-1	Sequence 1, Appli
c 20	49	1.4	3489	4	US-09-410-399-1	Sequence 1, Appli
21	49	1.4	32207	2	US-08-770-379-20	Sequence 20, Appl
22	49	1.4	32207	3	US-08-757-669A-20	Sequence 20, Appl
23	49	1.4	32207	4	US-09-230-371A-20	Sequence 20, Appl
24	48.4	1.4	1386	4	US-09-252-991A-11863	Sequence 11863, A
25	48.4	1.4	2304	4	US-09-252-991A-11802	Sequence 11802, A
26	47.4	1.4	2005	4	US-09-635-872A-18	Sequence 18, Appl
27	47.4	1.4	2005	4	US-09-636-077A-18	Sequence 18, Appl
28	47.4	1.4	2005	4	US-09-636-060C-18	Sequence 18, Appl
29	47.4	1.4	2005	4	US-09-986-552-18	Sequence 18, Appl
c 30	46.4	1.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli
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34	40.6	1.2	2144	3	US-08-834-306-15	Sequence 15, Appl
35	40.6	1.2	2144	3	US-08-993-674A-15	Sequence 15, Appl
36	40.6	1.2	2144	4	US-09-256-976-15	Sequence 15, Appl
37	40.2	1.2	13857	4	US-09-620-312D-75	Sequence 75, Appl
38	39.8	1.2	1383	4	US-09-635-872A-22	Sequence 22, Appl
39	39.8	1.2	1383	4	US-09-636-077A-22	Sequence 22, Appl
40	39.8	1.2	1383	4	US-09-636-060C-22	Sequence 22, Appl
41	39.8	1.2	1383	4	US-09-986-552-22	Sequence 22, Appl
42	39.8	1.2	2183	4	US-09-635-872A-7	Sequence 7, Appli
43	39.8	1.2	2183	4	US-09-636-077A-7	Sequence 7, Appli
44	39.8	1.2	2183	4	US-09-636-060C-7	Sequence 7, Appli
45	39.8	1.2	2183	4	US-09-986-552-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-09-130-491-9

; Sequence 9, Application US/09130491

; Patent No. 6416974

; GENERAL INFORMATION:

; APPLICANT: Holtzman, Douglas A.

; APPLICANT: Goodearl, Andrew D.J.

; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83

; FILE REFERENCE: 09404/041001

; CURRENT APPLICATION NUMBER: US/09/130,491

; CURRENT FILING DATE: 1998-08-07

; EARLIER APPLICATION NUMBER: US 60/058,108

; EARLIER FILING DATE: 1997-09-05

; EARLIER APPLICATION NUMBER: US 60/054,961

; EARLIER FILING DATE: 1997-08-06

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 9

; LENGTH: 1448
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-130-491-9

Query Match 41.7%; Score 1425.8; DB 4; Length 1448;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1427; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db	18	GGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTGTGACT	77
Qy	1276	GGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACCCCATGCCCTCTG	1335
Db	78	GGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACCCCATGCCCTCTG	137
Qy	1336	GGAACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAATGATGCAGTCTGCTCT	1395
Db	138	GGAACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAATGATGCAGTCTGCTCT	197
Qy	1396	CCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCACGGGGTGGACTGCTCCATCAGA	1455
Db	198	CCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCACGGGGTGGACTGCTCCATCAGA	257
Qy	1456	TGTCCCAGTGGCACATGGGGCTTTGGCTGTAACTTAACATGCCAGTGCCTCAACGGGGGA	1515
Db	258	TGTCCCAGTGGCACATGGGGCTTTGGCTGTAACTTAACATGCCAGTGCCTCAACGGGGGA	317
Qy	1516	GCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGGCGCGGGGAGAAATGC	1575
Db	318	GCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGGCGCGGGGAGAAATGC	377
Qy	1576	GAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAGCGCTGCGACTGCAGC	1635
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Qy	1636	CACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTCCCGGGATGGTCAGGT	1695
Db	438	CACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTCCCGGGATGGTCAGGT	497
Qy	1696	GTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAACTGCTCCCTGCCCTGC	1755
Db	498	GTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAACTGCTCCCTGCCCTGC	557
Qy	1756	TACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGCGAGTGTGCACCAGGC	1815
Db	558	TACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGCGAGTGTGCACCAGGC	617
Qy	1816	TTCCGAGGCACCACTTGTCTAGAGGATCTGCTCCCCTGGTTTTTATGGGCATCGCTGCAGC	1875
Db	618	TTCCGAGGCACCACTTGTCTAGAGGATCTGCTCCCCTGGTTTTTATGGGCATCGCTGCAGC	677
Qy	1876	CAGACATGCCACAGTGCCTTCACAGCAGCGGGCCCTGCCACCACATCACCGGCTGTGT	1935
Db	678	CAGACATGCCACAGTGCCTTCACAGCAGCGGGCCCTGCCACCACATCACCGGCTGTGT	737

Qy	1936	GACTGCTTGCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGTCCCAGTGGCAGATTT	1995
Db	738	GACTGCTTGCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGTCCCAGTGGCAGATTT	797
Qy	1996	GGGAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACCTGTAACCCCATTGAC	2055
Db	798	GGGAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACCTGTAACCCCATTGAC	857
Qy	2056	AGATCTTGTTCAGTGTACCCCGGTTGGATTGGCAGTGAAGTGTCTCAACCATGTCCACCT	2115
Db	858	AGATCTTGTTCAGTGTACCCCGGTTGGATTGGCAGTGAAGTGTCTCAACCATGTCCACCT	917
Qy	2116	GCCCACTGGGGCCCAAACCTGCATCCACACGTGCAACTGCCATAATGGAGCTTTCTGCAGC	2175
Db	918	GCCCACTGGGGCCCAAACCTGCATCCACACGTGCAACTGCCATAATGGAGCTTTCTGCAGC	977
Qy	2176	GCCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTCTACTGCACTCAGAGA	2235
Db	978	GCCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTCTACTGCACTCAGAGA	1037
Qy	2236	TGTCCTCTAGGGTTTTATGGAAAAGATTGTGCACTGATATGCCAATGTCAAACGGAGCT	2295
Db	1038	TGTCCTCTAGGGTTTTATGGAAAAGATTGTGCACTGATATGCCAATGTCAAACGGAGCT	1097
Qy	2296	GACTGCGACCACATTTCTGGGCAGTGTACTTGCCGCACTGGATTCATGGGACGGCACTGT	2355
Db	1098	GACTGCGACCACATTTCTGGGCAGTGTACTTGCCGCACTGGATTCATGGGACGGCACTGT	1157
Qy	2356	GAGCAGAAGTGGCCTTCAGGAACATATGGCTATGGCTGTGCGCCAGATATGTGATTGTCTG	2415
Db	1158	GAGCAGAAGTGGCCTTCAGGAACATATGGCTATGGCTGTGCGCCAGATATGTGATTGTCTG	1217
Qy	2416	AACAACCTCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGCCCCGGATGGAAGGGA	2475
Db	1218	AACAACCTCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGCCCCGGATGGAAGGGA	1277
Qy	2476	GCGAGATGTGATCAAGCTGGTGTATCATAGTTGGAAATCTGAACAGCTTAAGCCGAACC	2535
Db	1278	GCGAGATGTGATCAAGCTGGTGTATCATAGTTGGAAATCTGAACAGCTTAAGCCGAACC	1337
Qy	2536	AGTACTGCTCTCCCTGCTGATTCCTACCAGATCGGGGCCATTGCAGGCATCATCATTCTT	2595
Db	1338	AGTACTGCTCTCCCTGCTGATTCCTACCAAATCGGGGCCATTGCAGGCATCATCATTCTT	1397
Qy	2596	GTCCTAGTTGTTCTCTTCCCTACTGGCATTGTTTCATTATTTATAGACACA	2644
Db	1398	GTCCTAGTTGTTCTCTTCCCTACTGGCATTGTTTCATTATTTATAGACACA	1446

RESULT 2

US-09-833-381-1910/c

; Sequence 1910, Application US/09833381

; Patent No. 6672186

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs

; FILE REFERENCE: 5800-119

```
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1910
; LENGTH: 5197
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(5197)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1910
```

```
Query Match          15.3%; Score 524.6; DB 4; Length 5197;
Best Local Similarity 58.0%; Pred. No. 1.3e-152;
Matches 972; Conservative 0; Mismatches 694; Indels 11; Gaps 2;
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Qy      531 CTGCGAGGACCGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTG 590
      |||  | | |||  | |||  |||||  | |||  |  |||||
Db      4243 CTGCCTTCAGCCCTGTACCCCTGGCTACTATGGCCCTGCCTGCCAGTTCGGCTGCCAGTG 4184

Qy      591 CCAGAATGGAGCCACCTGCGACCACGTACGCGGGAATGCCGCTGCCCACCAGGATACAC 650
      ||  ||||  ||  |||||  | |  ||  ||  |||  |||||  |||  ||
Db      4183 CC---ATGGGGCACCCCTGCGATCCCCAGACTGGAGCCTGCTTCTGCCCCGAGAGAGAAC 4127

Qy      651 CGGAGCCTTCTGTGAGGATCTTTGTCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAG 710
      ||  ||  |||||  |  |||  | |  ||  ||  |||  ||  |
Db      4126 TGGGCCCAGCTGTGACGTGTCTGTTCAGGGCACTTCTGGCTTCTTCTGCCCCAGCAC 4067

Qy      711 ATGCCCTTGTCAAAATGGAGGAGTGTGTACACGTCACTGGAGAATGCTCTTGCCCTTC 770
      ||||  |||||  |||||  ||  | ||  |  ||  |||  ||||  |
Db      4066 CCATCCTTGCCAAAATGGAGGTGTCTTCAAACCCACAGGGCTCCTGCAGCTGCCCCC 4007

Qy      771 TGGCTGGATGGGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTG 830
      |||||  |||||  | ||  | |||  ||||  ||||  |||  ||||
Db      4006 TGGCTGGATGGGCACCATCTGCTCCCTGCCCTGCCAGAGGGCTTTCACGGACCCAACTG 3947

Qy      831 TTCCCAAGAATGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCA 890
      ||||  ||||  |  ||||  ||  ||  ||  ||||  |||  ||  ||  |
Db      3946 CTCCCAGGAATGTCGCTGCCACAACGGCGGCCTCTGTGACCGATTCACTGGGCAGTGCCG 3887

Qy      891 TTGCAGTCCAGGATACACAGGGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGG 950
      |||  ||  ||  ||||  ||||  |||||  ||  ||||  ||  ||  ||
Db      3886 CTGCGCTCCGGGTTACACTGGGGATCGGTGCCGGGAGGAGTGCCCGGTGGGCCGCTTTGG 3827

Qy      951 CGTTCTCTGTGCTGAGACCTGCCAGTGTGTCAACGGAGGGAAGTGTACCACGTGAGCGG 1010
      |||||  ||||  |||  | ||  |  |  |  ||  ||  ||  | |||
Db      3826 GCAGGACTGTGCTGAGACGTGCGACTGCGCCCCGACGCCCGTTGCTTCCCGGCCAACGG 3767

Qy      1011 CGCATGCCTCTGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCCTGA 1070
      ||||  ||  ||  ||  ||||  ||||  ||  ||||  |  ||||  ||  ||  ||
Db      3766 CGCATGTCTGTGCGAACACGGCTTCACTGGGGACCGCTGCACGGATCGCCTTGCCCCGA 3707

Qy      1071 GGGGCTCTACGGCATCAAATGTGACAAACGGTGTCCCTGCCACTTGGAACAACTCATAG 1130
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Db	3706	CGGCTTCTACGGTCTCAGCTGCCAGGCCCCCTGCACCTGCGACCGGGAGCACAGCCTCAG	3647
Qy	1131	CTGTCACCCCATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAA	1190
Db	3646	CTGCCACCCGATGAACGGGGAGTGTCTCCTGCCTGCCGGGTGGGCGGGCCTCCACTGCAA	3587
Qy	1191	TGAGACATGTTCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAA	1250
Db	3586	CGAGAGCTGCCCCGAGGACACGCATGGGCCAGGGTGCCAGGAGCACTGTCTCTGCCTGCA	3527
Qy	1251	TGGGGCAGACTGTGACAGTGTGACTGGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAAT	1310
Db	3526	CGGTGGCGTCTGCCAGGCTACCAGCGGCCTCTGTCACTGCGCGCCGGGTACACGGGCCC	3467
Qy	1311	TGACTGCTCTACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCTCTCGCTGTGG	1370
Db	3466	TCACTGTGCTAGTCTTTGTCTCCTCTGACACCTACGGTGTCAACTGTTCTGCACGCTGCTC	3407
Qy	1371	CTGTAAAAATGATGCACTCTGCTCTCCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTG	1430
Db	3406	ATGTGAAAATGCCATCGCCTGCTCACCCATCGACGGCGAGTGCCTCTGCAAGGAAGTTG	3347
Qy	1431	GCACGGGGTGGACTGCTCCATCAGATGTCCAGTGGCACATGGGGCTTTGGCTGTAACCT	1490
Db	3346	GCAGCGTGGTAACTGCTCTGTGCCCTGCCCACCCGGAACCTGGGGCTTCAGTTGCAATGC	3287
Qy	1491	AACATGCCAGTGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGC	1550
Db	3286	CAGCTGCCAGTGTGCCCATGAGGCAGTCTGCAGCCCCCAAACCTGGAGCCTGTACCTGCAC	3227
Qy	1551	ACCTGGATGGCGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAA	1610
Db	3226	CCCTGGGTGGCATGGGGCCCACTGCCAGCTGCCCTGTCCGAAGGGGCAGTTTGGAGAAGG	3167
Qy	1611	CTGTGCTGAGCGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTG	1670
Db	3166	TTGTGCCAGTCGCTGTGACTGTGACCACTCTGATGGCTGTGACCCTGTTTCATGGACGCTG	3107
Qy	1671	CCGCTGCCCTCCCGGGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTG	1730
Db	3106	TCAGTGCCAGGCTGGCTGGATGGGTGCCCCTGCCACCTGTCCTGCCCTGAGGGCTTATG	3047
Qy	1731	GGGCCCCAACTGCTCCCTGCCCTGCTACTGTAAAAATGGGGCTTCATGCTCCCTGATGA	1790
Db	3046	GGGAGTCAACTGTAGCAACACCTGCACCTGCAAGAATGGGGGCACCTGTCTCCCTGAGAA	2987
Qy	1791	TGGCATCTGCGAGTGTGCACCAGGCTTCCGAGGCACCACTTGTGAGAGGATCTGCTCCCC	1850
Db	2986	TGGCAACTGCGTGTGTGCACCCGGATTCCGGGGCCCCCTCCTGCCAGAGATCCTGTCAGCC	2927
Qy	1851	TGGTTTTTATGGGCATCGCTGCAGCCAGACATGCCACAGTGCCTTCACAGCAGCGGGCC	1910
Db	2926	TGGCCGCTATGGCAAACGCTGTG-----TGCCCTGCAAGTGCCTAACCCTCCTTC	2875
Qy	1911	CTGCCACCACATCACCGCCTGTGTGACTGCTTGCCCTGGCTTCACAGGCGCCCTCTGCAA	1970

Db 2874 TGCCACCCCTTCGAACGGGACCTGCTACTGCCTGGCTGGCTGGACAGGCCCCGACTGCTC 2815

Qy 1971 TGAAGTGTGTCCCACTGGCAGATTTGGGAAAACTGTGCAGGAATTTGTACCTGCACCAA 2030
 | | | | | | | | | | | | | | | | | | | | | |

Db 2814 CCAGCCATGCCCTCCAGGACACTGGGGAGAAAACTGTGCCAGACCTGCCAATGTCACCA 2755

Qy 2031 CAACGGAACCTGTAACCCCATTTGACAGATCTTGTCACTGTTACCCCGTTGGATTGGCAG 2090
 | | | | | | | | | | | | | | | | | | | | | |

Db 2754 TGGTGGGACCTGCCATCCCCAGGATGGGAGCTGTATCTGCCCCCTAGGCTGGACTGGACA 2695

Qy 2091 TGACTGCTCTCAACCATGTCCACCTGCCCACTGGGGCCCCAACTGCATCCACACGTGCAA 2150
 | | | | | | | | | | | | | | | | | | | | | |

Db 2694 CCACTGCTTAGAAGGCTGCCCTCTGGGGACATTTGGTGCTAACTGCTCCCAGCCATGCCA 2635

Qy 2151 CTGCCATAATGGAGCTTTCTGCAGCGCTACGATGGGGAATGTAAATGCACTCCTGG 2207
 | | | | | | | | | | | | | | | | | | | | | |

Db 2634 GTGTGGTCCTGGAGAAAAGTGCCACCCAGAGACTGGGGCCTGTGTATGTCCCCCAGG 2578

RESULT 3

US-09-130-491-10

; Sequence 10, Application US/09130491

; Patent No. 6416974

; GENERAL INFORMATION:

; APPLICANT: Holtzman, Douglas A.

; APPLICANT: Goodearl, Andrew D.J.

; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83

; FILE REFERENCE: 09404/041001

; CURRENT APPLICATION NUMBER: US/09/130,491

; CURRENT FILING DATE: 1998-08-07

; EARLIER APPLICATION NUMBER: US 60/058,108

; EARLIER FILING DATE: 1997-09-05

; EARLIER APPLICATION NUMBER: US 60/054,961

; EARLIER FILING DATE: 1997-08-06

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 10

; LENGTH: 1578

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(1578)

; OTHER INFORMATION: n = A,T,C or G

US-09-130-491-10

Query Match 4.8%; Score 165.8; DB 4; Length 1578;

Best Local Similarity 95.5%; Pred. No. 6e-41;

Matches 191; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

Qy 3227 AAGTTGAACCTACAGTGAGTGTGTGT--CCAAGGAGTATTTCAGCAATAATGGGCGTCTCTC 3284
 | | | | | | | | | | | | | | | | | | | | | |

Db 25 AAGTTGAACCTAACAGTGAGTGTGTGTTCCTCAAGGAGTATTTCAGCAATAATGGGCGTCTNTC 84

Qy 3285 CC-AGGATCCATATGACCTCCCAAAGAACAGTCACATCCCTTGTTCATTATGACCTGCTGC 3343
 | | | | | | | | | | | | | | | | | | | | | |

Db 85 CCAAGGATCCATATGACCTCCCAAAGAACAGTCACATCCCTTGTTCATTATGACCTGCTGC 144

```

QY      3344 CAGTCCGAGACAGTTCATCCTCCCCTAAGCAAGAGGACAGTGGAGGTAGCAGCAGCAACA 3403
          |||
Db      145  CAGTCCGAGACAGTTCATCCTCCCCTAAGCAAGAGGACAGTGGAGGTAGCAGCAGCAACA 204
          |||

QY      3404 GCAGCAGCAGCAGTGAATGA 3423
          |||
Db      205  GCAGCAGCAGCAGTGAATGA 224

```

US-09-188-930-255

; Patent No. 6150502

; APPLICANT: Watson, James D.

; APPLICANT: Sleeman, Matthew

: APPLICANT: Murison, James Greg

; TITLE OF INVENTION: and Methods For Their Use

; CURRENT APPLICATION NUMBER: US/09/188,930A

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; NUMBER OF SEQ ID NOS: 348

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; SEO ID NO 255

; TYPE: DNA

US-09-188-930-255

Best Local Similarity 51.2%; Pred. No. 6.5e-38;

Matches 419; Conservative 0; Mismatches 390; Indels 9; Gaps 2;

Qy 491 CCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGACCGCTGTGAGC 550
| | | | | | | | | | | | | | | | | | | | | |
Db 9 CGGGAGCCTGCTACTGCCCTGCTGGGTTTCCTTGGGGCCGACTGTAGCCTTGCCCTGTCCAC 68

QY 611 ACCACGTCACGGGGGAATGCCGCTGCCACCAGGATACACCGGAGCCTTCTGTGAGGATC 670
 ||| || |||| | || | | | | | | | | |
Db 129 ACCCAGTGTCGGGGACTTGCATCTGTCTCCCGGAAGACGGGAGGCCATTGTGAGCGCG 188

QY 731 GAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGATGGGCACAGTGT 790
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 249 GCCTGTGTCATGCTACCAATGGCAGCTGCTCCTGCCCCCTGGGCTGGATGGGGCCACACT 308

Qy 791 GTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAATGCCAGTGCC 850
 ||| || | |||| | || ||| ||| ||| ||| ||| |||
 Db 309 GTGAGCACGCCTGCCCTGCTGGGCGCTATGGTGTGCCTGCCTCCTGGAGTGTTCCTGTC 368

Qy 851 ATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCAGGATACACAG 910
 | || || | |||| | || | ||| || | || | || | || |
 Db 369 AGAACAATGGCAGCTGTGAGCCACCTCCGGCGCTTGCCTCTGTGGCCCTGGCTTCTATG 428

Qy 911 GGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGTGCTGAGACCT 970
 | || || | || | || ||| || | |||| | || |
 Db 429 GTCAAGCTTGTGAAGACACCTGCCCTGCCGGCTTCCATGGATCTGGTTGCCAGAGAGTTT 488

Qy 971 GCCAGTGTGTCAACGGAGGGAAGTGTACCACGTGAGCGGCGCATGCCTCTGTGAAGCAG 1030
 || |||| | || | || ||| || || ||| ||||| || |
 Db 489 GCGAGTGTCAACAGGGCGCTCCCTGTGACCTGTGAGTGCCCGGTGCCTCTGCCCTGCTG 548

Qy 1031 GCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCTGAGGGGCTCTACGGCATCAAAT 1090
 |||| |||| || |||| | || | || | || | || |
 Db 549 GCTTCCGTGGCCAGTTCTGCGAGAGGGG---GTGCAAGCCAGGCTTTTTTGGAGATGGCT 605

Qy 1091 GTGACAAACGGTGTCCCTGCCACTTGGAACACTCATAGCTGTCACCCCATGTCTGGAG 1150
 | | |||| |||| | || | |||| | |||| ||
 Db 606 GCCTGCAGCAGTGTAAGTACCCACGGGTGTGCC-----CTGTGATCCCATCAGCGGCC 659

Qy 1151 AGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGTTCTCCTGGAT 1210
 || |||| || || | |||| | || | || ||||
 Db 660 TCTGCCTTTGCCCCACCGGGCGCGCAGGAACCACATGTGACCTAGATTGCAGAAGAGGCC 719

Qy 1211 TCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTG 1270
 || || | || | || || | || |||| |||| ||||
 Db 720 GCTTTGGGCGGGCTGTGCCCTGCGCTGTGATTGTGGGGGTGGGGCTGACTGCGACCCCA 779

Qy 1271 TGACTGGAAAGTGACCTGTGCCCCAGGATTCAAAGGA 1308
 | | ||| |||| |||| | || ||||
 Db 780 TCAGTGGGCAGTGCCACTGTGTGGACAGCTACACGGGA 817

RESULT 5

US-09-312-283C-255

; Sequence 255, Application US/09312283C

; Patent No. 6573095

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Strachan, Lorna

; APPLICANT: Sleeman, Matthew

; APPLICANT: Onrust, Rene

; APPLICANT: Murison, James G.

; APPLICANT: Kumble, Krishanand D.

; TITLE OF INVENTION: Compositions Isolated from Skin Cells

; TITLE OF INVENTION: and Methods for Their Use

; FILE REFERENCE: 11000.1011c2

; CURRENT APPLICATION NUMBER: US/09/312,283C

; CURRENT FILING DATE: 1999-05-14

; NUMBER OF SEQ ID NOS: 425

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 255

; LENGTH: 1464

; TYPE: DNA
; ORGANISM: Mouse
US-09-312-283C-255

Query Match 4.6%; Score 156; DB 4; Length 1464;
Best Local Similarity 51.2%; Pred. No. 6.5e-38;
Matches 419; Conservative 0; Mismatches 390; Indels 9; Gaps 2;

```
Qy      491 CCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGACCGCTGTGAGC 550
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      9  CGGGAGCCTGCTACTGCCCTGCTGGGTTCTTGGGGCCGACTGTAGCCTTGCCCTGTCCAC 68

Qy     551 AGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATGGAGCCACCTGCG 610
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     69  AGGGTCGCTTCGGCCCCAGCTGTGCCACGTGTGTACATGCGGGCAAGGGGCGGCATGTG 128

Qy     611 ACCACGTCACGGGGGAATGCCGCTGCCACCAGGATACACCGGAGCCTTCTGTGAGGATC 670
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    129  ACCCAGTGTGCGGGGACTTGCATCTGTCTCCCGGGAAGACGGGAGGCCATTGTGAGCGCG 188

Qy     671 TTTGTCTCTCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGTCAAATGGAG 730
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    189  GCTGTCCCCAGGACCGGTTTGGCAAGGGCTGTGAACACAAGTGTGCCTGCAGGAATGGGG 248

Qy     731 GAGTGTGTCTACGTCACGTCAGTGGAGAATGCTCTTGCCCTTCTGGCTGGATGGGCACAGTGT 790
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    249  GCCTGTGTCTATGCTACCAATGGCAGCTGCTCCTGCCCCCTGGGCTGGATGGGGCCACACT 308

Qy     791 GTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAATGCCAGTGCC 850
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    309  GTGAGCACGCCTGCCCTGCTGGGCGCTATGGTGTCTGCCTGCCTCCTGGAGTGTTCCTGTC 368

Qy     851 ATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCAGGATACACAG 910
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    369  AGAACAATGGCAGCTGTGAGCCACCTCCGGCGCTTGCCCTCTGTGGCCCTGGCTTCTATG 428

Qy     911 GGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGTGCTGAGACCT 970
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    429  GTCAAGCTTGTGAAGACACCTGCCCTGCCGGCTTCCATGGATCTGGTTGCCAGAGAGTTT 488

Qy     971 GCCAGTGTGTCAACGGAGGGAAGTGTACCACGTGAGCGGCGCATGCCTCTGTGAAGCAG 1030
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    489  GCGAGTGTCAACAGGGCGCTCCCTGTGACCCTGTCAGTGGCCGGTGCCTCTGCCCTGCTG 548

Qy    1031 GCTTTGCTGGCGAGCGCTGCGAAGCACGCCCTGTGTCTGAGGGGCTCTACGGCATCAAAT 1090
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    549  GCTTCCGTGGCCAGTTCTGCGAGAGGGG---GTGCAAGCCAGGCTTTTTTGGAGATGGCT 605

Qy    1091 GTGACAAACGGTGTCCCTGCCACTTGGAACAACTCATAGCTGTACCCCATGTCTGGAG 1150
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    606  GCCTGCAGCAGTGTAACTGCCCCACGGGTGTGCC-----CTGTGATCCCATCAGCGGCC 659

Qy    1151 AGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGTTCTCCTGGAT 1210
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    660  TCTGCCTTTGCCACCAGGGCGCGCAGGAACCACATGTGACCTAGATTGCAGAAGAGGCC 719

Qy    1211 TCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTG 1270
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      || ||| | || | ||| || ||||| ||||| |||
Db      720 GCTTTGGGCCGGGCTGTGCCCTGCGCTGTGATTGTGGGGGTGGGGCTGACTGCGACCCCA 779

Qy      1271 TGACTGGAAAGTGACCTGTGCCCCAGGATTCAAAGGA 1308
      || ||| |||| |||| | || |||
Db      780 TCAGTGGGCAGTGCCACTGTGTGGACAGCTACACGGGA 817

```

RESULT 6

US-09-312-283C-73

; Sequence 73, Application US/09312283C

; Patent No. 6573095

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Strachan, Lorna

; APPLICANT: Sleeman, Matthew

; APPLICANT: Onrust, Rene

; APPLICANT: Murison, James G.

; APPLICANT: Kumble, Krishanand D.

; TITLE OF INVENTION: Compositions Isolated from Skin Cells

; TITLE OF INVENTION: and Methods for Their Use

; FILE REFERENCE: 11000.1011c2

; CURRENT APPLICATION NUMBER: US/09/312,283C

; CURRENT FILING DATE: 1999-05-14

; NUMBER OF SEQ ID NOS: 425

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 73

; LENGTH: 1635

; TYPE: DNA

; ORGANISM: Mouse

US-09-312-283C-73

Query Match 4.6%; Score 156; DB 4; Length 1635;

Best Local Similarity 51.2%; Pred. No. 7e-38;

Matches 419; Conservative 0; Mismatches 390; Indels 9; Gaps 2;

```

Qy      491 CCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGACCGCTGTGAGC 550
      | ||| || ||| |||| |||| || |||| || || ||| |||| |
Db      9 CGGGAGCCTGCTACTGCCCTGCTGGGTTCCCTTGGGGCCGACTGTAGCCTTGCCCTGTCCAC 68

Qy      551 AGGGCACCTATGGTAACGACTGTTCATCAGAGATGCCAGTGCCAGAATGGAGCCACCTGCG 610
      |||| || || | |||| || || || | || || || || || |
Db      69 AGGGTCGCTTCGGCCCCAGCTGTGCCACGTGTGTACATGCGGGCAAGGGGCGGCATGTG 128

Qy      611 ACCACGTACAGGGGGAATGCCGCTGCCCACCAGGATACACCGGAGCCTTCTGTGAGGATC 670
      ||| || |||| || || || || || || || || || || || ||
Db      129 ACCCAGTGTGCGGGGACTTGCATCTGTCTCCCGGGAAGACGGGAGGCCATTGTGAGCGCG 188

Qy      671 TTTGTCCTCCTGGTAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGTCAAAATGGAG 730
      ||||| | | ||| |||| || | || | || |||| |
Db      189 GCTGTCCCCAGGACCGGTTTGGCAAGGGCTGTGAACACAAGTGTGCCTGCAGGAATGGGG 248

Qy      731 GAGTGTGTTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGATGGGCACAGTGT 790
      | ||||| || || || |||| |||| ||||| || || |
Db      249 GCCTGTGTTCATGCTACCAATGGCAGCTGCTCCTGCCCCCTGGGCTGGATGGGGCCACACT 308

Qy      791 GTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAATGCCAGTGCC 850

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      |||  ||  | ||||  |  || ||||  |||  |||  ||  ||  ||  ||  ||
Db      309 GTGAGCACGCCTGCCCTGCTGGGCGCTATGGTGCTGCCTGCCTCCTGGAGTGTTCCTGTC 368

Qy      851 ATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCAGGATACACAG 910
      |  ||  ||  | ||||  |  ||  ||||  ||  ||  ||  ||  ||  ||  ||
Db      369 AGAACAATGGCAGCTGTGAGCCACCTCCGGCGCTTGCCCTCTGTGGCCCTGGCTTCTATG 428

Qy      911 GGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGTGCTGAGACCT 970
      |  ||  ||  | ||  ||  || ||||  ||  | ||||  |  ||  ||  ||
Db      429 GTCAAGCTTGTGAAGACACCTGCCCTGCCGGCTTCCATGGATCTGGTTGCCAGAGAGTTT 488

Qy      971 GCCAGTGTGTCAACGGAGGGAAGTGTACCACGTGAGCGGCGCATGCCTCTGTGAAGCAG 1030
      ||  ||||  |  ||  ||  || ||||  ||  || ||||  ||||  ||  ||
Db      489 GCGAGTGTCAACAGGGCGCTCCCTGTGACCTGTGAGTGGCCGGTGCCTCTGCCCTGCTG 548

Qy      1031 GCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCTGAGGGGCTCTACGGCATCAAAT 1090
      ||||  ||||  ||  ||||  |  |||  ||  ||  ||  ||  ||  ||  ||
Db      549 GCTTCCGTGGCCAGTTCTGCGAGAGGGG---GTGCAAGCCAGGCTTTTTTGGAGATGGCT 605

Qy      1091 GTGACAAACGGTGTCCCTGCCACTTGGAACAACTCATAGCTGTACCCCATGTCTGGAG 1150
      |  |  ||||  ||||  |  ||  |  ||||  ||||  ||  ||
Db      606 GCCTGCAGCAGTGTAAGTACCCACGGGTGTGCC-----CTGTGATCCCATCAGCGGCC 659

Qy      1151 AGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGTTCTCCTGGAT 1210
      ||  |||  ||  ||  |  ||||  |  ||||  ||  ||  ||
Db      660 TCTGCCTTTGCCACCAGGGCGCGCAGGAACCACATGTGACCTAGATTGCAGAAGAGGCC 719

Qy      1211 TCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTG 1270
      ||  |||  |  ||  ||  ||  ||  ||  ||||  ||||  ||
Db      720 GCTTTGGGCCGGGCTGTGCCCTGCGCTGTGATTGTGGGGGTGGGGCTGACTGCGACCCCA 779

Qy      1271 TGAAGTGGAAAGTGACCTGTGCCCCAGGATTCAAAGGA 1308
      |  |||  ||||  ||||  |  ||  ||  ||
Db      780 TCAGTGGGCAGTGCCACTGTGTGGACAGCTACACGGGA 817

```

RESULT 7

US-09-188-930-73

; Sequence 73, Application US/09188930A

; Patent No. 6150502

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Strachan, Lorna

; APPLICANT: Sleeman, Matthew

; APPLICANT: Onrust, Rene

; APPLICANT: Murison, James Greg

; TITLE OF INVENTION: Compositions Isolated From Skin Cells

; TITLE OF INVENTION: and Methods For Their Use

; FILE REFERENCE: 11000.1011c1

; CURRENT APPLICATION NUMBER: US/09/188,930A

; CURRENT FILING DATE: 1998-11-09

; NUMBER OF SEQ ID NOS: 348

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 73

; LENGTH: 1633

; TYPE: DNA

; ORGANISM: mouse

; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1608)...(1608)
US-09-188-930-73

Query Match 4.5%; Score 155.2; DB 3; Length 1633;
Best Local Similarity 51.0%; Pred. No. 1.2e-37;
Matches 417; Conservative 2; Mismatches 390; Indels 9; Gaps 2;

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Qy      491 CCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGACCGCTGTGAGC 550
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      9  CGGGAGCCTGCTACTGCCCTGCTGGGTTCCCTTGGGGCCGACTGTAGCCTTGCCTGTCCAC 68

Qy      551 AGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATGGAGCCACCTGCG 610
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      69 AGGGTCGCTTCGGCCCCAGCTGTGCCACGCTGTGTACATGCGGGCAAGGGGCGGCATGTG 128

Qy      611 ACCACGTCACGGGGGAATGCCGCTGCCACCAGGATACACCGGAGCCTTCTGTGAGGATC 670
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      129 ACCCAGTGTCGGGGACTTGCATCTGTCTCCCGGAAGACGGGAGGCCATTGTGAGCGCG 188

Qy      671 TTTGTCTCTCGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGTCAAATGGAG 730
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      189 GCTGTCCCAGGACCGGTTTGGCAAGGGCTGTGAACACAAGTGTGCCTGCAGGAATGGGG 248

Qy      731 GAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGATGGGCACAGTGT 790
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      249 GCCTGTGTCATGCTACCAATGGCAGCTGCTCCTGCCCTTGGCTGKATGGGGCCACACT 308

Qy      791 GTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAAATGCCAGTGCC 850
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      309 GTGAGCACGCCTGCCCTGCTGGGCGCTATGGTGCTGCCTGCCTCCTGGAGTGTTCCTGTC 368

Qy      851 ATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCAGGATACACAG 910
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      369 AGAACAATGGCAGCTGTGAGCCACCTCCGGCGCTTGCCTCTGTGGCCCTGGCTTCTATG 428

Qy      911 GGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGTGCTGAGACCT 970
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      429 GTCAAGCTTGTGAAGACACCTGCCCTGCCGGCTTCCATGGATCTGGTTGCCAGAGAGTTT 488

Qy      971 GCCAGTGTGTCAACGGAGGGAAGTGTACCACGTGAGCGGCGCATGCCTCTGTGAAGCAG 1030
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      489 GCGAGTGTCAACAGGGCGCTCCCTGTGACCCTGTCAGTGGCCGGTGCCTCTGCCCTGCTG 548

Qy      1031 GCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCTGAGGGGCTCTACGGCATCAAAT 1090
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      549 GCTTCCGTGGCCAGTTCTGCGAGAGGGG---GTGCAAGCCAGGCTTTTTTGGAGATGGCT 605

Qy      1091 GTGACAAACGGTGTCCCTGCCACTTGGAAAACACTCATAGCTGTCACCCCATGTCTGGAG 1150
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      606 GCCTGCAGCAGTGTAAGTACCCACGGGTGTGCC-----CTGTGATCCCATCAGCGGCC 659

Qy      1151 AGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGTTCTCCTGGAT 1210
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      660 TCTGCCTTTGCCACCAGGGCGCGCAGGAACACATGTGACCTAGATTGCAGAAGARGCC 719
```


Qy 1211 TCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTG 1270
 || ||| | || | || | || ||||| ||||| |||
 Db 720 GCTTTGGGCCGGGCTGTGCCCTGCGCTGTGATTGTGGGGGTGGGGCTGACTGCGACCCCA 779
 Qy 1271 TGACTGGAAAGTGCACCTGTGCCCCAGGATTCAAAGGA 1308
 | | ||| ||||| |||| | | || |||
 Db 780 TCAGTGGGCAGTGCCACTGTGTGGACAGCTACACGGGA 817

RESULT 8

US-09-833-381-1076

; Sequence 1076, Application US/09833381

; Patent No. 6672186

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs

; FILE REFERENCE: 5800-119

; CURRENT APPLICATION NUMBER: US/09/833,381

; CURRENT FILING DATE: 2001-04-11

; PRIOR APPLICATION NUMBER: 09/516,448

; PRIOR FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 2050

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1076

; LENGTH: 393

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-833-381-1076

Query Match 3.9%; Score 134.4; DB 4; Length 393;
 Best Local Similarity 61.9%; Pred. No. 1.4e-31;
 Matches 213; Conservative 0; Mismatches 131; Indels 0; Gaps 0;

Qy 781 GGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAA 840
 || ||||| ||||| |||| | ||| ||||| ||||| ||| ||
 Db 28 GGAGCAGTGTGTGCCAGCCCTGCCACCAGGGACATTTGGCCAGAAGTGCAGCCAGGAT 87
 Qy 841 TGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCA 900
 || | |||| | ||||| ||||| | || || || || || || |
 Db 88 TGTCTTGCCACCATGGAGGGCAGTGTGACCACGTGACTGGACAGTGCCACTGTACAGCT 147
 Qy 901 GGATACACAGGGGAACGGTGCCAGGATGAGTGTCTTGGGACCTATGGCGTTCTCTGT 960
 ||||| |||| | ||||| || |||| | || || || || || || ||
 Db 148 GGATACATGGGGGACAGGTGCCAAGAGGAGTGCCCTTCGGGTCTTCGGCTTCCAGTGC 207
 Qy 961 GCTGAGACCTGCCAGTGTGTCAACGGAGGGAAGTGTTACCACGTGAGCGGCGCATGCCTC 1020
 | || ||| | || ||| || ||| ||||| | | | || || |||
 Db 208 TCACAGCGCTGTGACTGCCACAATGGGGGGCAGTGTTACCCACCACGGGTGCCTGCGAG 267
 Qy 1021 TGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCCTGAGGGGCTCTAC 1080
 |||| | |||| ||| ||||| | | || |||| | || |||| || |
 Db 268 TGTGAGCCTGGCTACAAGGGCCACGCTGCCAGGAGCGACTGTGCCCGGAGGGCCTGCAT 327
 Qy 1081 GGCATCAAATGTGACAAACGGTGTCCCTGCCACTTGGAACAC 1124
 ||| || | | || |||| | || |||||
 Db 328 GGCCCAGGCTGCACCTGCCCTGCCCTGTGACGCTGACAACAC 371

RESULT 9

US-09-621-976-1192

; Sequence 1192, Application US/09621976
 ; Patent No. 6639063
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Jobert, S.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 ; FILE REFERENCE: GENSET.054PR2
 ; CURRENT APPLICATION NUMBER: US/09/621,976
 ; CURRENT FILING DATE: 2000-07-21
 ; NUMBER OF SEQ ID NOS: 19335
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 1192
 ; LENGTH: 553
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 331..552
 US-09-621-976-1192

Query Match 1.9%; Score 66.2; DB 4; Length 553;
 Best Local Similarity 60.1%; Pred. No. 3.6e-10;
 Matches 110; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy	2996	ACAGAAGCTATATGGGAAAATCCTTAAAAGACCTGGGAAAGAATTCTGAATATAATTCAA	3055
Db	347	ACACATACATTATGGACAAAGGCTTCAAAGATTACATGAAAGAATCCGTGTGCAGTTCTA	406
Qy	3056	GTAAGTCTCCCTAAGCAGTTCTGAGAACCCATATGCCACTATTAAAGACCCACCTGTAC	3115
Db	407	GTACTTGTTTCCTTGAATAGCAGTGAAAACCCCTTACGCCACAATTAAGGACCCACCCATCC	466
Qy	3116	TTATCCCGAAAAGCTCAGAGTGTGGTTATGTGGAGATGAAATCGCCGGCACGAAGAGATT	3175
Db	467	TCACCTGCAAGCTTCCAGAAAAGCAGCTATGTAGAAATGAAGTCGCCTGTGCACATGGGGT	526
Qy	3176	CCC	3178
Db	527	CTC	529

RESULT 10

US-08-323-474-1

; Sequence 1, Application US/08323474
 ; Patent No. 5447860
 ; GENERAL INFORMATION:
 ; APPLICANT: Ziegler, Steven F.
 ; TITLE OF INVENTION: NOVEL TYROSINE KINASE
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle

```

; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,474
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/905,600
; FILING DATE: 26-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2609
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4138 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 149..3523
US-08-323-474-1

```

```

Query Match          1.6%; Score 55.2; DB 1; Length 4138;
Best Local Similarity 60.8%; Pred. No. 4e-06;
Matches 90; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

```

```

Qy      1131 CTGTCACCCCATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAA 1190
        ||||| |||   |   | |||| ||||   | |||||   || ||   || ||
Db      985 CTGTCTCCCTGACCCCTATGGGTGTTCTGTGCCACAGGCTGGAAGGGTCTGCAGTGCAA 1044

Qy      1191 TGAGACATGTTCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAA 1250
        |||  ||||   ||||| || |||||   || |||   |||  |  ||||| ||| ||
Db      1045 TGAAGCATGCCACCCTGGTTTTTACGGGCCAGATTGTAAGCTTAGGTGCAGCTGCAACAA 1104

Qy      1251 TGGGGCAGACTGTGACAGTGTGACTGGA 1278
        |||||   ||||| | |   |||
Db      1105 TGGGGAGATGTGTGATCGCTTCCAAGGA 1132

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RESULT 11
PCT-US93-06093-1
; Sequence 1, Application PC/TUS9306093
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Steven F.

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; TITLE OF INVENTION: NOVEL TYROSINE KINASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06093
; FILING DATE: 19930625
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/905,600
; FILING DATE: 26-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2609
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4138 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 149..3523
PCT-US93-06093-1

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Query Match          1.6%; Score 55.2; DB 5; Length 4138;
Best Local Similarity 60.8%; Pred. No. 4e-06;
Matches 90; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

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Qy      1131 CTGTCACCCCATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAA 1190
        ||||| |||      |      | |||| ||||      | |||||      || || | || ||
Db      985 CTGTCTCCCTGACCCCTATGGGTGTTCTGTGCCACAGGCTGGAAGGGTCTGCAGTGCAA 1044

Qy      1191 TGAGACATGTTCTCTCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAA 1250
        |||  ||||      ||||| || |||||      || |||  |||  | ||||| || | ||
Db      1045 TGAAGCATGCCACCTGGTTTTTTACGGGCCAGATTGTAAGCTTAGGTGCAGCTGCAACAA 1104

Qy      1251 TGGGGCAGACTGTGACAGTGTGACTGGA 1278
        |||||      ||||| | |  |||
Db      1105 TGGGGAGATGTGTGATCGCTTCCAAGGA 1132

```

RESULT 12

US-08-220-240A-4

; Sequence 4, Application US/08220240A

; Patent No. 5955291

; GENERAL INFORMATION:

; APPLICANT: Alitalo, Kari

; APPLICANT: Matikainen, Marja-Terttu

; APPLICANT: Partanen, Juha

; APPLICANT: Makela, Tomi

; APPLICANT: Korhonen, Jaana

; TITLE OF INVENTION: ANTIBODIES RECOGNIZING TIE RECEPTOR

; TITLE OF INVENTION: TYROSINE KINASE AND USES THEREOF

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 233 South Wacker Drive/6300 Sears Tower

; CITY: Chicago

; STATE: Illinois

; COUNTRY: Unites States of America

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/220,240A

; FILING DATE: 29-MAR-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/FI93/00006

; FILING DATE: 08-JAN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/817,800

; FILING DATE: 09-JAN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/167,453

; FILING DATE: 15-DEC-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Gass, David A.

; REGISTRATION NUMBER: 38,153

; REFERENCE/DOCKET NUMBER: 29151/31958

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 474-6300

; TELEFAX: (312) 474-0448

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3845 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 37..3450

US-08-220-240A-4

Query Match 1.6%; Score 54; DB 2; Length 3845;
 Best Local Similarity 51.4%; Pred. No. 9e-06;
 Matches 179; Conservative 0; Mismatches 160; Indels 9; Gaps 2;

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Qy      1709 GCGTGTGTGCTGAGGGACGCTGGGGCCCCAACTGCTCCCTGCCCTGC---TACTGTAAAA 1765
          | |  |||  |  || |||||  ||  ||  ||  |  ||  ||  |
Db      674 GGGGTTGTGGGGCTGGGCGCTGGGGGCCAGGCTGTACCAAGGAGTGCCAGGTTGCCTAC 733

Qy      1766 ATGGGGCTTCATGCTCCCCTGATGATGGCATCTGCGAGTGTGCACCAGGCTTCCGAGGCA 1825
          |||  |  |  |||  |  |||  ||  ||  |  |  ||  |||  |||
Db      734 ATGGAGGTGTCTGCCACGACCATGACGGCGAATGTGTATGCCCCCTGGCTTCACTGGCA 793

Qy      1826 CCACTTGTGAGAGGATCTGCTCCCCTGGTTTTTATGGGCATCGCTGCAGCCAGACATGCC 1885
          ||  |||  |  |  |||  ||  ||  |||  |||  |||  ||  |||
Db      794 CCCGCTGTGAACAGGCCTGCAGAGAGGGCCGTTTGGGCAGAGCTGCCAGGAGCAGTGCC 853

Qy      1886 CACAGTGCCTTCACAGCAGCGGGCCCTGCCACCACATCACCGGCCTGTGTGACTGCTTGC 1945
          ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      854 CAGGCATATCAGGCTGCCGGGGCCTCACCTTCTGCCTCCCAGACCCCTATGGCTGCTCTT 913

Qy      1946 -----CTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGTCCCAGTGGCAGATTGGGA 1999
          |||  |||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      914 GTGGATCTGGCTGGAGAGGAAGCCAGTGCCAAGAAGCTTGTGCCCCTGGTCATTTGGGG 973

Qy      2000 AAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACCTGTAACC 2047
          |  ||  |  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      974 CTGATTGCCGACTCCAGTGCCAGTGTGAGAATGGTGGCACTTGTGACC 1021
  
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RESULT 13

US-07-934-393B-1

; Sequence 1, Application US/07934393B

; Patent No. 5466596

; GENERAL INFORMATION:

; APPLICANT: BREITMAN, MARTIN L.

; APPLICANT: DUMONT, DANIEL

; APPLICANT: GRADWOHL, GERARD G.

; TITLE OF INVENTION: TISSUE SPECIFIC TRANSCRIPTIONAL

; TITLE OF INVENTION: REGULATORY ELEMENT

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BERESKIN & PARR

; STREET: 40 King Street West

; CITY: Toronto

; STATE: Ontario

; COUNTRY: Canada

; ZIP: M5H 3Y2

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/934,393B

; FILING DATE: 25-AUG-1992

; CLASSIFICATION: 435

```

; ATTORNEY/AGENT INFORMATION:
;   NAME:  Kurdydyk, Linda M.
;   REGISTRATION NUMBER:  34,971
;   REFERENCE/DOCKET NUMBER:  3153-64
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (416) 354-7311
;   TELEFAX:  (416) 361-1398
; INFORMATION FOR SEQ ID NO:  1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH:  4175 base pairs
;   TYPE:  nucleic acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
; MOLECULE TYPE:  cDNA
; HYPOTHETICAL:  NO
; ANTI-SENSE:  NO
; FRAGMENT TYPE:  N-terminal
; ORIGINAL SOURCE:
;   ORGANISM:  Mus pahari
;   STRAIN:  CD-1
;   DEVELOPMENTAL STAGE:  Embryo
;   TISSUE TYPE:  Heart
; IMMEDIATE SOURCE:
;   CLONE:  tek
; POSITION IN GENOME:
;   CHROMOSOME/SEGMENT:  4
;   MAP POSITION:  Between the brown and pmv-23 loci
; FEATURE:
;   NAME/KEY:  CDS
;   LOCATION:  124..3477
;   OTHER INFORMATION:  /function= "putative transmembrane
;   OTHER INFORMATION:  receptor"
;   OTHER INFORMATION:  /product= "tyrosine kinase"
;   OTHER INFORMATION:  /gene= "tek"
;   OTHER INFORMATION:  /standard_name= "tyrosine kinase receptor protein"
US-07-934-393B-1

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Query Match          1.6%;  Score 54;  DB 1;  Length 4175;
Best Local Similarity 50.6%;  Pred. No. 9.6e-06;
Matches 166;  Conservative 0;  Mismatches 150;  Indels 12;  Gaps 1;

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Qy      716 CTTGTCAAAATGGAGGAGTGTGTTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCT 775
        |||| | || |||| | || | | | | | | | | | | | | | | |
Db      800 CTTGCAAGAACAATGGAGTCTGCCATGAAGATACCGGGGAATGCATTTGCCCTCCTGGGT 859

Qy      776 GGATGGGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCC 835
        |||| | | ||| | |||| | | |||| | | ||||
Db      860 TTATGGGGAGAACATGTGAGAAAGCTTGTGAGCCGCACACATTTGGCAGGACCTGTAAAG 919

Qy      836 AAGAATGCCAGTGCCATAATGGAGGGACGTGTGATG-----CTGCCACAGGCC 883
        || || | | | ||| | | || | || | | | | | | | | |
Db      920 AAAGGTGTAGTGGACCAAGAAGGATGCAAGTCTTATGTGTTCTGTCTCCAGACCCTTACG 979

Qy      884 AATGTCATTGCAGTCCAGGATACACAGGGGAACGGTGCCAGGATGAGTGTCTGTTGGGA 943
        ||| || |||| | | ||| | |||| | || | || | |||
Db      980 GGTGTTCTGTGCCACAGGCTGGAGGGGGTTGCAGTGCAATGAAGCATGCCCATCTGGTT 1039

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Qy 944 CCTATGGCGTTCTCTGTGCTGAGACCTGCCAGTGTGTCAACGGAGGGAAGTGTACCACG 1003
 ||| || |||| | |||| ||| ||| | ||| ||| |||
 Db 1040 ACTACGGACCAGACTGTAAGCTCAGGTGCCACTGTACCAATGAAGAGATATGTGATCGGT 1099
 Qy 1004 TGAGCGGCGCATGCCTCTGTGAAGCAGG 1031
 | || | ||| | |
 Db 1100 TCCAAGGATGCCTCTGCTCTCAAGGATG 1127

RESULT 14

US-08-278-089A-1

; Sequence 1, Application US/08278089A

; Patent No. 5681714

; GENERAL INFORMATION:

; APPLICANT: Breitman, Martin L.

; APPLICANT: Rossant, Janet

; APPLICANT: Dumont, Daniel J.

; APPLICANT: Yamaguchi, Terry P.

; TITLE OF INVENTION: No. 5681714e1 Receptor Tyrosine Kinase

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Bereskin & Parr

; STREET: 40 King Street West

; CITY: Toronto

; STATE: Ontario

; COUNTRY: Canada

; ZIP: M5H 3Y2

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/278,089A

; FILING DATE: 20-JUL-1994

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Kurdydyk, Linda M.

; REGISTRATION NUMBER: 34,971

; REFERENCE/DOCKET NUMBER: 3153-111

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (416) 364-7311

; TELEFAX: (416) 361-1398

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4175 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: N-terminal

; ORIGINAL SOURCE:

; ORGANISM: Mus musculus

; STRAIN: CD-1

; DEVELOPMENTAL STAGE: Embryo


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; TISSUE TYPE: Heart
; IMMEDIATE SOURCE:
; CLONE: Tek
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 4
; MAP POSITION: Between the brown and pmv-23 loci
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..3478
US-08-278-089A-1

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Best Local Similarity 50.6%; Pred. No. 9.6e-06;
Matches 166; Conservative 0; Mismatches 150; Indels 12; Gaps 1;

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; Sequence 1, Application US/08838957A

; Patent No. 5998187

; GENERAL INFORMATION:

; APPLICANT: Breitman, Martin L.

; APPLICANT: Rossant, Janet

; APPLICANT: Dumont, Daniel J.

; APPLICANT: Yamaguchi, Terry P.

; TITLE OF INVENTION: No. 5998187e1 Receptor Tyrosine Kinase

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Bereskin & Parr

; STREET: 40 King Street West

; CITY: Toronto

; STATE: Ontario

; COUNTRY: Canada

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; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,957A
; FILING DATE: 23-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M.
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4175 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; STRAIN: CD-1
; DEVELOPMENTAL STAGE: Embryo
; TISSUE TYPE: Heart
; IMMEDIATE SOURCE:
; CLONE: Tek
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 4
; MAP POSITION: Between the brown and pmv-23 loci
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; NAME/KEY: CDS
; LOCATION: 124..3478
US-08-838-957A-1

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Best Local Similarity 50.6%; Pred. No. 9.6e-06;
Matches 166; Conservative 0; Mismatches 150; Indels 12; Gaps 1;

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Job time : 269 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 30, 2004, 02:15:41 ; Search time 1109 Seconds
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Perfect score: 3423
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2458946 seqs, 1861504846 residues

Total number of hits satisfying chosen parameters: 4917892

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	1760	51.4	1761	14	US-10-092-390-3	Sequence 3, Appli
4	1425.8	41.7	1448	13	US-10-105-929-9	Sequence 9, Appli
5	1425.8	41.7	1448	14	US-10-365-227-9	Sequence 9, Appli
6	640.6	18.7	3114	15	US-10-052-648A-9	Sequence 9, Appli
7	635.8	18.6	5000	15	US-10-052-648A-7	Sequence 7, Appli
8	608.4	17.8	3567	10	US-09-796-753-99	Sequence 99, Appl
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15	511	14.9	3063	15	US-10-052-648A-1	Sequence 1, Appli
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30	156	4.6	1464	10	US-09-866-050A-255	Sequence 255, App
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ALIGNMENTS

RESULT 1

US-10-092-390-1

; Sequence 1, Application US/10092390

; Publication No. US20030013865A1

; GENERAL INFORMATION:

; APPLICANT: Yu, Xuanchuan

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; APPLICANT: Miranda, Maricar
; TITLE OF INVENTION: No. US20030013865A1el Human EGF-Family Proteins and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0317-USA
; CURRENT APPLICATION NUMBER: US/10/092,390
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US 60/275,013
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3423
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-092-390-1

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	2401	ATATGTGATTGTCTGAACAACTCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGC	2460
Qy	2461	CCCGGATGGAAGGGAGCGAGATGTGATCAAGCTGGTGTATCATAGTTGGAAATCTGAAC	2520
Db	2461	CCCGGATGGAAGGGAGCGAGATGTGATCAAGCTGGTGTATCATAGTTGGAAATCTGAAC	2520
Qy	2521	AGCTTAAGCCGAACCACTGCTCTCCCTGCTGATTCTACCAGATCGGGGCCATTGCA	2580
Db	2521	AGCTTAAGCCGAACCACTGCTCTCCCTGCTGATTCTACCAGATCGGGGCCATTGCA	2580
Qy	2581	GGCATCATCATTCTTGTCTAGTTGTTCTCTTCTACTGGCATTGTTTCATTATTTATAGA	2640
Db	2581	GGCATCATCATTCTTGTCTAGTTGTTCTCTTCTACTGGCATTGTTTCATTATTTATAGA	2640
Qy	2641	CACAAGCAGAAGGGAAAGGAATCAAGCATGCCAGCAGTTACCTACACCCCTGCTATGAGG	2700
Db	2641	CACAAGCAGAAGGGAAAGGAATCAAGCATGCCAGCAGTTACCTACACCCCTGCTATGAGG	2700
Qy	2701	GTCGTCAATGCAGATTATACCATTTTCAGGAACCCCTCCTCACAGCAATGGTGGAAACGCT	2760
Db	2701	GTCGTCAATGCAGATTATACCATTTTCAGGAACCCCTCCTCACAGCAATGGTGGAAACGCT	2760
Qy	2761	AATAGCCACTACTTCACCAATCCCAGTTACCACACGCTCACCCAGTGTCACACATCCCCT	2820
Db	2761	AATAGCCACTACTTCACCAATCCCAGTTACCACACGCTCACCCAGTGTCACACATCCCCT	2820
Qy	2821	CACGTCAACAACAGGGACAGGATGACTGTCACGAAGTCAAAAAACAATCAACTGTTTGTG	2880
Db	2821	CACGTCAACAACAGGGACAGGATGACTGTCACGAAGTCAAAAAACAATCAACTGTTTGTG	2880
Qy	2881	AATCTTAAAAATGTGAACCCTGGGAAGAGAGGCCCTGTGGGGGACTGCACTGGGACATTG	2940
Db	2881	AATCTTAAAAATGTGAACCCTGGGAAGAGAGGCCCTGTGGGGGACTGCACTGGGACATTG	2940
Qy	2941	CCGGCTGACTGGAAACATGGCGGCTACCTCAACGAGCTCGGTGCTTTTGGACTTGACAGA	3000
Db	2941	CCGGCTGACTGGAAACATGGCGGCTACCTCAACGAGCTCGGTGCTTTTGGACTTGACAGA	3000
Qy	3001	AGCTATATGGGAAAATCCTTAAAAGACCTGGGAAAGAATTCTGAATATAATTCAAGTAAC	3060
Db	3001	AGCTATATGGGAAAATCCTTAAAAGACCTGGGAAAGAATTCTGAATATAATTCAAGTAAC	3060
Qy	3061	TGCTCCCTAAGCAGTTCTGAGAACCCATATGCCACTATTAAAGACCCACCTGTACTTATC	3120
Db	3061	TGCTCCCTAAGCAGTTCTGAGAACCCATATGCCACTATTAAAGACCCACCTGTACTTATC	3120

Qy 3121 CCGAAAAGCTCAGAGTGTGGTTATGTGGAGATGAAATCGCCGGCACGAAGAGATTCCCCA 3180
 |||
 Db 3121 CCGAAAAGCTCAGAGTGTGGTTATGTGGAGATGAAATCGCCGGCACGAAGAGATTCCCCA 3180

Qy 3181 TATGCAGAGATCAATAACTCAACTTCAGCCAACAGGAATGTCTATGAAGTTGAACCTACA 3240
 |||
 Db 3181 TATGCAGAGATCAATAACTCAACTTCAGCCAACAGGAATGTCTATGAAGTTGAACCTACA 3240

Qy 3241 GTGAGTGTGTCCAAGGAGTATTTCAGCAATAATGGGCGTCTCTCCAGGATCCATATGAC 3300
 |||
 Db 3241 GTGAGTGTGTCCAAGGAGTATTTCAGCAATAATGGGCGTCTCTCCAGGATCCATATGAC 3300

Qy 3301 CTCCCAAAGAACAGTCACATCCCTTGTTCATTATGACCTGCTGCCAGTCCGAGACAGTTCA 3360
 |||
 Db 3301 CTCCCAAAGAACAGTCACATCCCTTGTTCATTATGACCTGCTGCCAGTCCGAGACAGTTCA 3360

Qy 3361 TCCTCCCCTAAGCAAGAGGACAGTGGAGGTAGCAGCAGCAACAGCAGCAGCAGTGA 3420
 |||
 Db 3361 TCCTCCCCTAAGCAAGAGGACAGTGGAGGTAGCAGCAGCAACAGCAGCAGCAGTGA 3420

Qy 3421 TGA 3423
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 Db 3421 TGA 3423

RESULT 2

US-10-365-227-19

; Sequence 19, Application US/10365227

; Publication No. US20030143632A1

; GENERAL INFORMATION:

; APPLICANT: McCarthy, Sean A.

; APPLICANT: Holtzman, Douglas A.

; APPLICANT: Goodearl, Andrew D.J.

; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING

; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC AND

OTHER

; TITLE OF INVENTION: USES

; FILE REFERENCE: 07334-323001

; CURRENT APPLICATION NUMBER: US/10/365,227

; CURRENT FILING DATE: 2003-02-12

; PRIOR APPLICATION NUMBER: US/09/802,582

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: US 09/128,709

; PRIOR FILING DATE: 1998-08-04

; PRIOR APPLICATION NUMBER: US 60/054,645

; PRIOR FILING DATE: 1997-08-04

; PRIOR APPLICATION NUMBER: US 09/130,491

; PRIOR FILING DATE: 1998-08-06

; PRIOR APPLICATION NUMBER: US 60/054,966

; PRIOR FILING DATE: 1997-08-06

; PRIOR APPLICATION NUMBER: US 60/058,108

; PRIOR FILING DATE: 1997-09-05

; PRIOR APPLICATION NUMBER: US 09/388,280

; PRIOR FILING DATE: 1999-09-01

; PRIOR APPLICATION NUMBER: US 09/388,279

; PRIOR FILING DATE: 1999-09-01

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 3552
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1803)
US-10-365-227-19

Query Match 64.1%; Score 2192.8; DB 14; Length 3552;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2205; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy      1216 GGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTGTGACT 1275
          |||
Db        1 GGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTGTGACT 60

Qy      1276 GGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACCCCATGCCCTCTG 1335
          |||
Db        61 GGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACCCCATGCCCTCTG 120

Qy      1336 GGAACCTATGGGATAAACTGTTTCCTCTCGCTGTGGCTGTAAAAATGATGCAGTCTGCTCT 1395
          |||
Db       121 GGAACCTATGGGATAAACTGTTTCCTCTCGCTGTGGCTGTAAAAATGATGCAGTCTGCTCT 180

Qy      1396 CCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCACGGGGTGGACTGCTCCATCAGA 1455
          |||
Db       181 CCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCACGGGGTGGACTGCTCCATCAGA 240

Qy      1456 TGTCCCAGTGGCACATGGGGCTTTGGCTGTAACTTAACATGCCAGTGCCTCAACGGGGGA 1515
          |||
Db       241 TGTCCCAGTGGCACATGGGGCTTTGGCTGTAACTTAACATGCCAGTGCCTCAACGGGGGA 300

Qy      1516 GCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGGCGCGGGGAGAAATGC 1575
          |||
Db       301 GCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGGCGCGGGGAGAAATGC 360

Qy      1576 GAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAGCGCTGCGACTGCAGC 1635
          |||
Db       361 GAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAGCGCTGCGACTGCAGC 420

Qy      1636 CACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTCCCGGGATGGTCAGGT 1695
          |||
Db       421 CACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTCCCGGGATGGTCAGGT 480

Qy      1696 GTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAACTGCTCCCTGCCCTGC 1755
          |||
Db       481 GTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAACTGCTCCCTGCCCTGC 540

Qy      1756 TACTGTAAAAATGGGGCTTCATGCTCCCTGATGATGGCATCTGCGAGTGTGCACCAGGC 1815
          |||
Db       541 TACTGTAAAAATGGGGCTTCATGCTCCCTGATGATGGCATCTGCGAGTGTGCACCAGGC 600

Qy      1816 TTCCGAGGCACCACTTGTGAGAGGATCTGCTCCCTGGTTTTATGGGCATCGCTGCAGC 1875
          |||
Db       601 TTCCGAGGCACCACTTGTGAGAGGATCTGCTCCCTGGTTTTATGGGCATCGCTGCAGC 660
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Qy	1876	CAGACATGCCCACAGTGC GTTCACAGCAGCGGGCCCTGCCACCACATCACCGGCCTGTGT	1935
Db	661	CAGACATGCCCACAGTGC GTTCACAGCAGCGGGCCCTGCCACCACATCACCGGCCTGTGT	720
Qy	1936	GACTGCTTGCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGTCCCAGTGGCAGATTT	1995
Db	721	GACTGCTTGCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGTCCCAGTGGCAGATTT	780
Qy	1996	GGGAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACCTGTAACCCCATTGAC	2055
Db	781	GGGAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACCTGTAACCCCATTGAC	840
Qy	2056	AGATCTTGTCA GTGTTACCCCGGTTGGATTGGCAGTGA CTGCTCTCAACCATGTCCACCT	2115
Db	841	AGATCTTGTCA GTGTTACCCCGGTTGGATTGGCAGTGA CTGCTCTCAACCATGTCCACCT	900
Qy	2116	GCCCACTGGGGCCCAA ACTGCATCCACACGTGCAACTGCCATAATGGAGCTTTCTGCAGC	2175
Db	901	GCCCACTGGGGCCCAA ACTGCATCCACACGTGCAACTGCCATAATGGAGCTTTCTGCAGC	960
Qy	2176	GCCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTCTACTGCACTCAGAGA	2235
Db	961	GCCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTCTACTGCACTCAGAGA	1020
Qy	2236	TGTCCTCTAGGGTTTTATGGAAAAGATTGTGCACTGATATGCCAATGTCAAAACGGAGCT	2295
Db	1021	TGTCCTCTAGGGTTTTATGGAAAAGATTGTGCACTGATATGCCAATGTCAAAACGGAGCT	1080
Qy	2296	GACTGCGACCACATTTCTGGGCAGTGTACTTGCCGCAC TGGATTTCATGGGACGGCACTGT	2355
Db	1081	GACTGCGACCACATTTCTGGGCAGTGTACTTGCCGCAC TGGATTTCATGGGACGGCACTGT	1140
Qy	2356	GAGCAGAAGTGCCCTTCAGGAACATATGGCTATGGCTGT CGCCAGATATGTGATTGTCTG	2415
Db	1141	GAGCAGAAGTGCCCTTCAGGAACATATGGCTATGGCTGT CGCCAGATATGTGATTGTCTG	1200
Qy	2416	AACAAC TCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGCCCCGGATGGAAGGGA	2475
Db	1201	AACAAC TCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGCCCCGGATGGAAGGGA	1260
Qy	2476	GCGAGATGTGATCAAGCTGGTGTATCATAGTTGGAAATCTGAACAGCTTAAGCCGAACC	2535
Db	1261	GCGAGATGTGATCAAGCTGGTGTATCATAGTTGGAAATCTGAACAGCTTAAGCCGAACC	1320
Qy	2536	AGTACTGCTCTCCCTGCTGATTCTTACCAGATCGGGGCCATTGCAGGCATCATCATTCTT	2595
Db	1321	AGTACTGCTCTCCCTGCTGATTCTTACCACATCGGGGCCATTGCAGGCATCATCATTCTT	1380
Qy	2596	GTCCTAGTTGTTCTCTTCTACTGGCATTGTTTATTATTTATAGACACAAGCAGAAGGGA	2655
Db	1381	GTCCTAGTTGTTCTCTTCTACTGGCATTGTTTATTATTTATAGACACAAGCAGAAGGGA	1440
Qy	2656	AAGGAATCAAGCATGCCAGCAGTTACCTACACCCCTGCTATGAGGGTCGTCAATGCAGAT	2715
Db	1441	AAGGAATCAAGCATGCCAGCAGTTACCTACACCCCTGCTATGAGGGTCGTCAATGCAGAT	1500

Qy 2716 TATACCATTTCAGGAACCCCTTCCTCACAGCAATGGTGGAAACGCTAATAGCCACTACTTC 2775
 |||
 Db 1501 TATACCATTTCAGGAACCCCTTCCTCACAGCAATGGTGGAAACGCTAATAGCCACTACTTC 1560

Qy 2776 ACCAATCCCAGTTACCACACGCTCACCCAGTGTGCCACATCCCCTCACGTCAACAACAGG 2835
 |||
 Db 1561 ACCAATCCCAGTTACCACACGCTCACCCAGTGTGCCACATCCCCTCACGTCAACAACAGG 1620

Qy 2836 GACAGGATGACTGTCACGAAGTCAAAAAACAATCAACTGTTTGTGAATCTTAAAAATGTG 2895
 |||
 Db 1621 GACAGGATGACTGTCACGAAGTCAAAAAACAATCAACTGTTTGTGAATCTTAAAAATGTG 1680

Qy 2896 AACCCTGGGAAGAGAGGCCCTGTGGGGGACTGCACTGGGACATTGCCGGCTGACTGGAAA 2955
 |||
 Db 1681 AACCCTGGGAAGAGAGGCCCTGTGGGGGACTGCA-TGGGACATTGCCGGCTGACTGGAAA 1739

Qy 2956 CATGGCGGCTACCTCAACGAGCTCGGTGCTTTTGGACTTGACAGAAGCTATATGGGAAAA 3015
 |||
 Db 1740 CATGGCGGCTACCTCAACGAGCTCGGTGCTTTTGGACTTGACAGAAGCTATATGGGAAAA 1799

Qy 3016 TCCTTAAAAGACCTGGGAAAGAATTCTGAATATAATTCAAGTAAGTCTCCCTAAGCAGT 3075
 |||
 Db 1800 TCCTTAAAAGACCTGGGAAAGAATTCTGAATATAATTCAAGTAAGTCTCCCTAAGCAGT 1859

Qy 3076 TCTGAGAACCCATATGCCACTATTAAAGACCCACCTGTACTTATCCCGAAAAGCTCAGAG 3135
 |||
 Db 1860 TCTGAGAACCCATATGCCACTATTAAAGACCCACCTGTACTTATCCCGAAAAGCTCAGAG 1919

Qy 3136 TGTGGTTATGTGGAGATGAAATCGCCGGCAGGAAGAGATTCCCATATGCAGAGATCAAT 3195
 |||
 Db 1920 TGTGGTTATGTGGAGATGAAATCGCCGGCAGGAAGAGATTCCCATATGCAGAGATCAAT 1979

Qy 3196 AACTCAACTTCAGCCAACAGGAATGTCTATGAAGTTGAACCTACAGTGAGTGTGTCCAA 3255
 |||
 Db 1980 AACTCAACTTCAGCCAACAGGAATGTCTATGAAGTTGAACCTACAGTGAGTGTGTCCAA 2039

Qy 3256 GGAGTATTTCAGCAATAATGGGCGTCTCTCCAGGATCCATATGACCTCCCAAAGAACAGT 3315
 |||
 Db 2040 GGAGTATTTCAGCAATAATGGGCGTCTCTCCAGGATCCATATGACCTCCCAAAGAACAGT 2099

Qy 3316 CACATCCCTTGTCTATTATGACCTGCTGCCAGTCCGAGACAGTTCATCCTCCCCTAAGCAA 3375
 |||
 Db 2100 CACATCCCTTGTCTATTATGACCTGCTGCCAGTCCGAGACAGTTCATCCTCCCCTAAGCAA 2159

Qy 3376 GAGGACAGTGGAGGTAGCAGCAGCAACAGCAGCAGCAGCAGTGAATGA 3423
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 Db 2160 GAGGACAGTGGAGGTAGCAGCAGCAACAGCAGCAGCAGCAGTGAATGA 2207

RESULT 3

US-10-092-390-3

; Sequence 3, Application US/10092390

; Publication No. US20030013865A1

; GENERAL INFORMATION:

; APPLICANT: Yu, Xuanchuan

; APPLICANT: Miranda, Maricar

```
; TITLE OF INVENTION: No. US20030013865A1 Human EGF-Family Proteins and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0317-USA
; CURRENT APPLICATION NUMBER: US/10/092,390
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US 60/275,013
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-092-390-3
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Query Match          51.4%; Score 1760; DB 14; Length 1761;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1760; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 ATGGTTATTTCTTTGAACTCATGCCTGAGCTTTATTTGTTTATTGTTATGCCACTGGATT 60
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Db      1 ATGGTTATTTCTTTGAACTCATGCCTGAGCTTTATTTGTTTATTGTTATGCCACTGGATT 60

Qy     61 GGGACAGCATCACCTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTAC 120
      |||
Db     61 GGGACAGCATCACCTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTAC 120

Qy    121 TCAGTGACTGTGCAAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGC 180
      |||
Db    121 TCAGTGACTGTGCAAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGC 180

Qy    181 ACTGACATTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCTAT 240
      |||
Db    181 ACTGACATTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCTAT 240

Qy    241 CGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTGTCCTGGATTTTATGAA 300
      |||
Db    241 CGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTGTCCTGGATTTTATGAA 300

Qy    301 AGCGGGGAAATGTGTGTCCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTGCT 360
      |||
Db    301 AGCGGGGAAATGTGTGTCCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTGCT 360

Qy    361 CCAAACACCTGTCAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGAT 420
      |||
Db    361 CCAAACACCTGTCAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGAT 420

Qy    421 GGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGC 480
      |||
Db    421 GGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGC 480

Qy    481 AACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGAC 540
      |||
Db    481 AACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGAC 540

Qy    541 CGCTGTGAGCAGGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATGGA 600
      |||
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Db	541	CGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATGGA	600
Qy	601	GCCACCTGCGACCACGTACGCGGGGAATGCCGCTGCCCACCAGGATACACCGGAGCCTTC	660
Db	601	GCCACCTGCGACCACGTACGCGGGGAATGCCGCTGCCCACCAGGATACACCGGAGCCTTC	660
Qy	661	TGTGAGGATCTTTGTCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGT	720
Db	661	TGTGAGGATCTTTGTCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGT	720
Qy	721	CAAAATGGAGGAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGATG	780
Db	721	CAAAATGGAGGAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGATG	780
Qy	781	GGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAA	840
Db	781	GGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAA	840
Qy	841	TGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCA	900
Db	841	TGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCA	900
Qy	901	GGATACACAGGGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGT	960
Db	901	GGATACACAGGGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGT	960
Qy	961	GCTGAGACCTGCCAGTGTGTCAACGGAGGGAAGTGTACCACGTGAGCGGCGCATGCCTC	1020
Db	961	GCTGAGACCTGCCAGTGTGTCAACGGAGGGAAGTGTACCACGTGAGCGGCGCATGCCTC	1020
Qy	1021	TGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCTGAGGGGCTCTAC	1080
Db	1021	TGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCTGAGGGGCTCTAC	1080
Qy	1081	GGCATCAAATGTGACAAACGGTGTCCCTGCCACTTGGAACAACTCATAGCTGTCACCCC	1140
Db	1081	GGCATCAAATGTGACAAACGGTGTCCCTGCCACTTGGAACAACTCATAGCTGTCACCCC	1140
Qy	1141	ATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGT	1200
Db	1141	ATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGT	1200
Qy	1201	TCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGAC	1260
Db	1201	TCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGAC	1260
Qy	1261	TGTGACAGTGTGACTGGAAAGTGACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCT	1320
Db	1261	TGTGACAGTGTGACTGGAAAGTGACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCT	1320
Qy	1321	ACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAAT	1380
Db	1321	ACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAAT	1380
Qy	1381	GATGCAGTCTGCTCTCCTGTGGACGGGTCTTGACTTGCAAGGCAGGCTGGCACGGGGTG	1440
Db	1381	GATGCAGTCTGCTCTCCTGTGGACGGGTCTTGACTTGCAAGGCAGGCTGGCACGGGGTG	1440

Qy 1441 GACTGCTCCATCAGATGTCCCAGTGGCACATGGGGCTTTGGCTGTAACTTAACATGCCAG 1500
 |||
 Db 1441 GACTGCTCCATCAGATGTCCCAGTGGCACATGGGGCTTTGGCTGTAACTTAACATGCCAG 1500

Qy 1501 TGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGG 1560
 |||
 Db 1501 TGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGG 1560

Qy 1561 CGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAG 1620
 |||
 Db 1561 CGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAG 1620

Qy 1621 CGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTC 1680
 |||
 Db 1621 CGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTC 1680

Qy 1681 CCGGGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAAC 1740
 |||
 Db 1681 CCGGGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAAC 1740

Qy 1741 TGCTCCCTGCCCTGCTACTG 1760
 |||
 Db 1741 TGCTCCCTGCCCTGCTACTG 1760

RESULT 4

US-10-105-929-9

; Sequence 9, Application US/10105929

; Publication No. US20020137142A1

; GENERAL INFORMATION:

; APPLICANT: Holtzman, Douglas A.

; APPLICANT: Goodearl, Andrew D.J.

; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83

; FILE REFERENCE: 09404/041001

; CURRENT APPLICATION NUMBER: US/10/105,929

; CURRENT FILING DATE: 2002-03-25

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,491

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,108

; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/054,961

; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 9

; LENGTH: 1448

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-105-929-9

Query Match 41.7%; Score 1425.8; DB 13; Length 1448;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1427; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1216 GGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTGTGACT 1275
 |||

Db 18 GGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTGTGACT 77

Qy 1276 GGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACCCCATGCCCTCTG 1335
 |||

Db 78 GGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACCCCATGCCCTCTG 137

Qy 1336 GGAACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAATGATGCAGTCTGCTCT 1395
 |||

Db 138 GGAACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAATGATGCAGTCTGCTCT 197

Qy 1396 CCTGTGGACGGGTCTTGACTTGCAAGGCAGGCTGGCACGGGGTGGACTGCTCCATCAGA 1455
 |||

Db 198 CCTGTGGACGGGTCTTGACTTGCAAGGCAGGCTGGCACGGGGTGGACTGCTCCATCAGA 257

Qy 1456 TGTCCCAGTGGCACATGGGGCTTTGGCTGTAACCTTAACATGCCAGTGCCTCAACGGGGGA 1515
 |||

Db 258 TGTCCCAGTGGCACATGGGGCTTTGGCTGTAACCTTAACATGCCAGTGCCTCAACGGGGGA 317

Qy 1516 GCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGGCGCGGGGAGAAATGC 1575
 |||

Db 318 GCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGGCGCGGGGAGAAATGC 377

Qy 1576 GAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAGCGCTGCGACTGCAGC 1635
 |||

Db 378 GAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAGCGCTGCGACTGCAGC 437

Qy 1636 CACGCAGATGGCTGCCACCCTACCACGGGGCCATTGCCGCTGCCTCCCCGGATGGTCAGGT 1695
 |||

Db 438 CACGCAGATGGCTGCCACCCTACCACGGGGCCATTGCCGCTGCCTCCCCGGATGGTCAGGT 497

Qy 1696 GTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAACTGCTCCCTGCCCTGC 1755
 |||

Db 498 GTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAACTGCTCCCTGCCCTGC 557

Qy 1756 TACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGCGAGTGTGCACCAGGC 1815
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Db 558 TACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGCGAGTGTGCACCAGGC 617

Qy 1816 TTCCGAGGCACCACTTGTCAGAGGATCTGCTCCCCTGGTTTTTATGGGCATCGCTGCAGC 1875
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Db 618 TTCCGAGGCACCACTTGTCAGAGGATCTGCTCCCCTGGTTTTTATGGGCATCGCTGCAGC 677

Qy 1876 CAGACATGCCCACAGTGCCTTACAGCAGCGGGCCCTGCCACCACATCACGGGCCTGTGT 1935
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Db 678 CAGACATGCCCACAGTGCCTTACAGCAGCGGGCCCTGCCACCACATCACGGGCCTGTGT 737

Qy 1936 GACTGCTTGCCTGGCTTACAGGCGCCCTCTGCAATGAAGTGTGTCCAGTGGCAGATTT 1995
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Db 738 GACTGCTTGCCTGGCTTACAGGCGCCCTCTGCAATGAAGTGTGTCCAGTGGCAGATTT 797

Qy 1996 GGGAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACCTGTAACCCCATTTGAC 2055
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Db 798 GGGAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACCTGTAACCCCATTTGAC 857

Qy 2056 AGATCTTGTCAAGTGTACCCCGGTTGGATTGGCAGTGAAGTGTGTCCAGTGGCAGATTT 2115
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Db 858 AGATCTTGTCAAGTGTACCCCGGTTGGATTGGCAGTGAAGTGTGTCCAGTGGCAGATTT 917

QY 2116 GCCCACTGGGGCCCAAACCTGCATCCACACGTGCAACTGCCATAATGGAGCTTTCTGCAGC 2175
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 Db 918 GCCCACTGGGGCCCAAACCTGCATCCACACGTGCAACTGCCATAATGGAGCTTTCTGCAGC 977
 QY 2176 GCCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTCTACTGCACTCAGAGA 2235
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 Db 978 GCCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTCTACTGCACTCAGAGA 1037
 QY 2236 TGTCTCTAGGGTTTTATGGAAAAGATTGTGCACTGATATGCCAATGTCAAAACGGAGCT 2295
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 Db 1038 TGTCTCTAGGGTTTTATGGAAAAGATTGTGCACTGATATGCCAATGTCAAAACGGAGCT 1097
 QY 2296 GACTGCGACCACATTTCTGGGCAGTGACTTGCCGCACTGGATTTCATGGGACGGCACTGT 2355
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 Db 1098 GACTGCGACCACATTTCTGGGCAGTGACTTGCCGCACTGGATTTCATGGGACGGCACTGT 1157
 QY 2356 GAGCAGAAGTGCCCTTCAGGAACATATGGCTATGGCTGTGCGCCAGATATGTGATTGTCTG 2415
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 Db 1158 GAGCAGAAGTGCCCTTCAGGAACATATGGCTATGGCTGTGCGCCAGATATGTGATTGTCTG 1217
 QY 2416 AACAACTCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGCCCCGGATGGAAGGGA 2475
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 Db 1218 AACAACTCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGCCCCGGATGGAAGGGA 1277
 QY 2476 GCGAGATGTGATCAAGCTGGTGTTATCATAGTTGGAAATCTGAACAGCTTAAGCCGAACC 2535
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 Db 1278 GCGAGATGTGATCAAGCTGGTGTTATCATAGTTGGAAATCTGAACAGCTTAAGCCGAACC 1337
 QY 2536 AGTACTGCTCTCCCTGCTGATTCCTACCAGATCGGGGCCATTGCAGGCATCATCATTCTT 2595
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 Db 1338 AGTACTGCTCTCCCTGCTGATTCCTACCAAATCGGGGCCATTGCAGGCATCATCATTCTT 1397
 QY 2596 GTCCTAGTTGTTCTCTTCCTACTGGCATTGTTTCATTATTTATAGACACA 2644
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 Db 1398 GTCCTAGTTGTTCTCTTCCTACTGGCATTGTTTCATTATTTATAGACACA 1446

RESULT 5

US-10-365-227-9

; Sequence 9, Application US/10365227

; Publication No. US20030143632A1

; GENERAL INFORMATION:

; APPLICANT: McCarthy, Sean A.

; APPLICANT: Holtzman, Douglas A.

; APPLICANT: Goodearl, Andrew D.J.

; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING

; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC AND
 OTHER

; TITLE OF INVENTION: USES

; FILE REFERENCE: 07334-323001

; CURRENT APPLICATION NUMBER: US/10/365,227

; CURRENT FILING DATE: 2003-02-12

; PRIOR APPLICATION NUMBER: US/09/802,582

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: US 09/128,709

; PRIOR FILING DATE: 1998-08-04

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; PRIOR APPLICATION NUMBER: US 60/054,645
; PRIOR FILING DATE: 1997-08-04
; PRIOR APPLICATION NUMBER: US 09/130,491
; PRIOR FILING DATE: 1998-08-06
; PRIOR APPLICATION NUMBER: US 60/054,966
; PRIOR FILING DATE: 1997-08-06
; PRIOR APPLICATION NUMBER: US 60/058,108
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 09/388,280
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: US 09/388,279
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1448
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-365-227-9

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Query Match          41.7%; Score 1425.8; DB 14; Length 1448;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1427; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1216 GGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTGTGACT 1275
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Db      18   GGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTGTGACT 77

Qy      1276 GGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACCCCATGCCCTCTG 1335
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Db      78   GGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACCCCATGCCCTCTG 137

Qy      1336 GGAACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAATGATGCAGTCTGCTCT 1395
          |||
Db      138  GGAACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAATGATGCAGTCTGCTCT 197

Qy      1396 CCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCACGGGGTGGACTGCTCCATCAGA 1455
          |||
Db      198  CCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCACGGGGTGGACTGCTCCATCAGA 257

Qy      1456 TGTCCCACTGGCACATGGGGCTTTGGCTGTAACTTAACATGCCAGTGCCTCAACGGGGGA 1515
          |||
Db      258  TGTCCCACTGGCACATGGGGCTTTGGCTGTAACTTAACATGCCAGTGCCTCAACGGGGGA 317

Qy      1516 GCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGGCGCGGGGAGAAATGC 1575
          |||
Db      318  GCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGGCGCGGGGAGAAATGC 377

Qy      1576 GAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAGCGCTGCGACTGCAGC 1635
          |||
Db      378  GAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAGCGCTGCGACTGCAGC 437

Qy      1636 CACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTCCCGGGATGGTCAGGT 1695
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Db      438  CACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTCCCGGGATGGTCAGGT 497

Qy      1696 GTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAACTGCTCCCTGCCCTGC 1755

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Db	498		GTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAACTGCTCCCTGCCCTGC	557
Qy	1756		TACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGCGAGTGTGCACCAGGC	1815
Db	558		TACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGCGAGTGTGCACCAGGC	617
Qy	1816		TTCCGAGGCACCACTTGTCTCAGAGGATCTGCTCCCCGGTTTTTATGGGCATCGCTGCAGC	1875
Db	618		TTCCGAGGCACCACTTGTCTCAGAGGATCTGCTCCCCGGTTTTTATGGGCATCGCTGCAGC	677
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Db	678		CAGACATGCCCACAGTGCCTTCACAGCAGCGGGCCCTGCCACCACATCACCGGCCTGTGT	737
Qy	1936		GACTGCTTGCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGTCCCAGTGGCAGATTT	1995
Db	738		GACTGCTTGCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGTCCCAGTGGCAGATTT	797
Qy	1996		GGGAAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACCTGTAACCCCATTTGAC	2055
Db	798		GGGAAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACCTGTAACCCCATTTGAC	857
Qy	2056		AGATCTTGTCTAGTGTACCCCGTTGGATTGGCAGTGACTGCTCTCAACCATGTCCACCT	2115
Db	858		AGATCTTGTCTAGTGTACCCCGTTGGATTGGCAGTGACTGCTCTCAACCATGTCCACCT	917
Qy	2116		GCCCACTGGGGCCCCAACTGCATCCACACGTGCAACTGCCATAATGGAGCTTTCTGCAGC	2175
Db	918		GCCCACTGGGGCCCCAACTGCATCCACACGTGCAACTGCCATAATGGAGCTTTCTGCAGC	977
Qy	2176		GCCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTCTACTGCACTCAGAGA	2235
Db	978		GCCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTCTACTGCACTCAGAGA	1037
Qy	2236		TGTCCTCTAGGGTTTTATGGAAAAGATTGTGCACTGATATGCCAATGTCAAACGGAGCT	2295
Db	1038		TGTCCTCTAGGGTTTTATGGAAAAGATTGTGCACTGATATGCCAATGTCAAACGGAGCT	1097
Qy	2296		GACTGCGACCACATTTCTGGGCAGTGTACTTGCCGCACTGGATTTCATGGGACGGCACTGT	2355
Db	1098		GACTGCGACCACATTTCTGGGCAGTGTACTTGCCGCACTGGATTTCATGGGACGGCACTGT	1157
Qy	2356		GAGCAGAAGTGCCCTTCAGGAACATATGGCTATGGCTGTGCGCCAGATATGTGATTGTCTG	2415
Db	1158		GAGCAGAAGTGCCCTTCAGGAACATATGGCTATGGCTGTGCGCCAGATATGTGATTGTCTG	1217
Qy	2416		AACAACCTCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGCCCCGGATGGAAGGGA	2475
Db	1218		AACAACCTCCACCTGCGACCACATCACTGGGACCTGTTACTGCAGCCCCGGATGGAAGGGA	1277
Qy	2476		GCGAGATGTGATCAAGCTGGTGTATCATAGTTGGAAATCTGAACAGCTTAAGCCGAACC	2535
Db	1278		GCGAGATGTGATCAAGCTGGTGTATCATAGTTGGAAATCTGAACAGCTTAAGCCGAACC	1337
Qy	2536		AGTACTGCTCTCCCTGCTGATTCTTACCAGATCGGGGCCATTGCAGGCATCATCATTCTT	2595

Db 1338 AGTACTGCTCTCCCTGCTGATTCCCTACCAAATCGGGGCCATTGCAGGCATCATCATTCTT 1397

QY 2596 GTCCTAGTTGTTCTCTTCTACTGGCATTGTTTCATTATTTATAGACACA 2644
|||||

Db 1398 GTCCTAGTTGTTCTCTTCTACTGGCATTGTTTCATTATTTATAGACACA 1446

RESULT 6

US-10-052-648A-9

; Sequence 9, Application US/10052648A

; Publication No. US20040005558A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, David

; APPLICANT: Burgess, Catherine

; APPLICANT: Casman, Stacie

; APPLICANT: Colman, Steven

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Ellerman, Karen

; APPLICANT: Gerlach, Valerie

; APPLICANT: Gunther, Erik

; APPLICANT: Kekuda, Ramesh

; APPLICANT: MacDougall, John R.

; APPLICANT: Mehraban, Fuad

; APPLICANT: Patturajan, Meera

; APPLICANT: Rothenberg, Mark

; APPLICANT: Shimkets, Richard

; APPLICANT: Smithson, Glennda

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Stone, David J.

; APPLICANT: Vernet, Corine A.M.

; APPLICANT: Zerhusen, Bryan D.

; TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF

; TITLE OF INVENTION: USING THE SAME

; FILE REFERENCE: 21402-250 (CURA-550)

; CURRENT APPLICATION NUMBER: US/10/052,648A

; CURRENT FILING DATE: 2002-12-09

; PRIOR APPLICATION NUMBER: 60/262,454

; PRIOR FILING DATE: 2001-01-18

; PRIOR APPLICATION NUMBER: 60/272,920

; PRIOR FILING DATE: 2001-03-02

; PRIOR APPLICATION NUMBER: 60/284,549

; PRIOR FILING DATE: 2001-04-18

; PRIOR APPLICATION NUMBER: 60/303,229

; PRIOR FILING DATE: 2001-07-05

; PRIOR APPLICATION NUMBER: 60/262,892

; PRIOR FILING DATE: 2001-01-19

; PRIOR APPLICATION NUMBER: 60/263,605

; PRIOR FILING DATE: 2001-01-23

; PRIOR APPLICATION NUMBER: 60/269,098

; PRIOR FILING DATE: 2001-02-15

; PRIOR APPLICATION NUMBER: 60/264,159

; PRIOR FILING DATE: 2001-01-25

; PRIOR APPLICATION NUMBER: 60/265,517

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/271,855

; PRIOR FILING DATE: 2001-02-27

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3114
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-648A-9

Query Match 18.7%; Score 640.6; DB 15; Length 3114;
Best Local Similarity 57.5%; Pred. No. 1.6e-196;
Matches 1235; Conservative 0; Mismatches 899; Indels 15; Gaps 4;

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Qy      62 GGACAGCATCACCTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTACT 121
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Db      47 GGCTGGCTGGAACCTCTCAACCCAGTGATCCCAATACCTGCAGCTTCTGGGAAAGCTTCA 106

Qy     122 CAGTGACTGTGCAAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGC- 180
      |  ||  | |||| || | | |||| |  |  ||  | |||| 
Db     107 CTACCACCACCAAGGAGTCCCAGTCCCAGCCCTTCAGCCTGCTCCCCTCAGAGCCCTGCG 166

Qy     181 --ACTGACATTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCT 238
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Db     167 AGCGGCCCTGGGAGGGCCCCCATACTTGCCCCCAGCCACGGTTGTATACCGGACCGTGT 226

Qy     239 ATCGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTGTCCCTGGATTTTATG 298
      | || || | || |||||  | | |  |||| | | ||| || |||| 
Db     227 ACCGTCAGGTGGTGAAGACGGACCACCGCCAGCGCCTGCAGTGTGCCATGGCTTCTATG 286

Qy     299 AAAGCGGGGAAATGTGTGTCCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTG 358
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Db     287 AGAGCAGGGAGTTCTGTGTCCCGCTCTGTGCCCAGGAGTGTGTCCATGGCCGTTGTGTGG 346

Qy     359 CTCCAAACACCTGTGAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCG 418
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Db     347 CACCCAATCAGTGCCAATGTGTGCCAGGCTGGCGGGGCGACGACTGTTCCAGTGAGTGTG 406

Qy     419 ATGGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGT 478
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Db     407 CCCCAGGAATGTGGGGGCCACAGTGTGACAAGCCCTGCAGTTGCGGCAACAACAGCTCGT 466

Qy     479 GCAACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGG 538
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Db     467 GTGATCCCAAGAGTGGGGTATGTTCTTGCCCTTCTGGTCTGCAGCCCCCGAACTGCCTTC 526

Qy     539 ACCGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATG 598
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Db     527 AGCCCTGTACCCCTGGCTACTATGGCCCTGCCTGCCAGTTCGCTGCCAGTGCC---ATG 583

Qy     599 GAGCCACCTGCGACCACGTACGGGGGAATGCCGCTGCCACCAGGATACACCGGAGCCT 658
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Db     584 GGGCACCTGCGATCCCCAGACTGGAGCCTGCTTCTGCCCCGAGAGAGAACTGGGCCCA 643

Qy     659 TCTGTGAGGATCTTTGTCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTT 718
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Db     644 GCTGTGACGTGTCCTGTTCCCAGGGCACTTCTGGCTTCTTCTGCCCCAGCACCCATCCTT 703

Qy     719 GTCAAAATGGAGGAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGA 778
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Db	764	TGGGCACCATCTGCTCCCTGCCCTGCCAGAGGGCTTTACGGACCCAACTGCTCCCAGG	823
Qy	839	AATGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTC	898
Db	824	AATGTCGCTGCCACAACGGCGGCCTCTGTGACCGATTCACTGGGCAGTGCCGCTGCGCTC	883
Qy	899	CAGGATACACAGGGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCT	958
Db	884	CGGGTTACACTGGGGATCGGTGCCGGGAGGAGTGCCCGGTGGGCCGCTTTGGGCAGGACT	943
Qy	959	GTGCTGAGACCTGCCAGTGTGTCAACGGAGGGGAAGTGTTACCACGTGAGCGGCGCATGCC	1018
Db	944	GTGCTGAGACGTGCGACTGCGCCCCGGACGCCCGTTGCTTCCCGGCCAACGGCGCATGTC	1003
Qy	1019	TCTGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCTGAGGGGCTCT	1078
Db	1004	TGTGCGAACACGGCTTCACTGGGGACCGCTGCACGGATCGCCTCTGCCCCGACGGCTTCT	1063
Qy	1079	ACGGCATCAAATGTGACAAACGGTGTCCCTGCCACTTGGAACAACTCATAGCTGTCACC	1138
Db	1064	ACGGTCTCAGCTGCCAGGCCCCCTGCACCTGCGACCGGGAGCACAGCCTCAGCTGCCACC	1123
Qy	1139	CCATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACAT	1198
Db	1124	CGATGAACGGGGAGTGCTCCTGCCTGCCGGGCTGGGCGGGCCTCCACTGCAACGAGAGCT	1183
Qy	1199	GTTCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAG	1258
Db	1184	GCCCGCAGGACACGCATGGGCCAGGGTGCCAGGAGTACTGTCTCTGCCTGCACGGTGGCG	1243
Qy	1259	ACTGTGACAGTGTGACTGGAAAGTGACCTGTGCCCCAGGATTCAAAGGAATTGACTGCT	1318
Db	1244	TCTGCCAGGCTACCAGCGGCCTCTGTCACTGCGCGCCGGGTTACAGGGCCCTCACTGTG	1303
Qy	1319	CTACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTTCTCTCGCTGTGGCTGTAAAA	1378
Db	1304	CTAGTCTTTGTCTCTGACACCTACGGTGTCAACTGTTCTGCACGCTGCTCATGTGAAA	1363
Qy	1379	ATGATGCAGTCTGCTCTCCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCACGGGG	1438
Db	1364	ATGCCATCGCCTGCTCACCCATCGACGGCGAGTGCGTCTGCAAGGAAGGTTGGCAGCGTG	1423
Qy	1439	TGGACTGCTCCATCAGATGTCCCAGTGGCACATGGGGCTTTGGCTGTAACCTTAACATGCC	1498
Db	1424	GTAACCTGCTCTGTGCCCTGCCACCCGGAACCTGGGGCTTCAGTTGCAATGCCAGCTGCC	1483
Qy	1499	AGTGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGAT	1558
Db	1484	AGTGTGCCCATGAGGCAGTCTGCAGCCCCAACTGGAGCCTGTACCTGCACCCCTGGGT	1543
Qy	1559	GGCGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTG	1618

Db 1544 GGCATGGGGCCCACTGCCAGCTGCCCTGTCCGAAGGGGCAGTTTGGAGAAGGTTGTGCCA 1603
 Qy 1619 AGCGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGGCCATTGCCGCTGCC 1678
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 Db 1604 GTCGCTGTGACTGTGACCACTCTGATGGCTGTGACCCTGTTTCATGGACGCTGTCAGTGCC 1663
 Qy 1679 TCCCGGGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCA 1738
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 Db 1664 AGGCTGGCTGGATGGGTGCCCCTGCCACCTGTCCTGCCCTGAGGGCTTATGGGGAGTCA 1723
 Qy 1739 ACTGCTCCCTGCCCTGCTACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCT 1798
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 Db 1724 ACTGTAGCAACACCTGCACCTGCAAGAATGGGGGCACCTGTCTCCCTGAGAATGGCAACT 1783
 Qy 1799 GCGAGTGTGCACCAGGCTTCCGAGGCACCACTTGTGACAGGATCTGCTCCCCTGGTTTTT 1858
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 Db 1784 GCGTGTGTGCACCCGGATTCCGGGGCCCCCTCCTGCCAGAGATCCTGTCAGCCTGGCCGCT 1843
 Qy 1859 ATGGGCATCGCTGCAGCCAGACATGCCCACAGTGCCTTCACAGCAGCGGGCCCTGCCACC 1918
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 Db 1844 ATGGCAAACGCTGTGTGC-----CCTGCAAGTGCCTAACCCTCC---TTCTGCCACC 1894
 Qy 1919 ACATCACCGGCCTGTGTGACTGCTTGCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGT 1978
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 Db 1895 CCTCGAACGGGACCTGCTACTGCCTGGCTGGCTGGACAGGCCCCGACTGCTCCCAGCCAT 1954
 Qy 1979 GTCCCACTGGCAGATTTGGGAAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAA 2038
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 Db 1955 GCCCTCCAGGACACTGGGGAGAAAACTGTGCCAGACCTGCCAATGTCACCATGGTGGGA 2014
 Qy 2039 CCTGTAACCCCATTTGACAGATCTTGTGAGTGTACCCCGGTTGGATTGGCAGTGACTGCT 2098
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 Db 2015 CCTGCCATCCCCAGGATGGGAGCTGTATCTGCCCCCTAGGCTGGACTGGACACCACTGCT 2074
 Qy 2099 CTCAACCATGTCCACCTGCCCCTGGGGCCCCAACTGCATCCACACGTGCAACTGCCATA 2158
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 Db 2075 TAGAAGGCTGCCCTCTGGGGACATTTGGTGCTAACTGCTCCCAGCCATGCCAGTGTGGTC 2134
 Qy 2159 ATGGAGCTTTCTGCAGCGCCTACGATGGGGAATGTAAATGCACTCCTGG 2207
 ||||| ||| || | |||| || || || || ||
 Db 2135 CTGGAGAAAAGTGCCACCCAGAGACTGGGGCCTGTGTATGTCCCCCAGG 2183

RESULT 7

US-10-052-648A-7

; Sequence 7, Application US/10052648A

; Publication No. US20040005558A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, David

; APPLICANT: Burgess, Catherine

; APPLICANT: Casman, Stacie

; APPLICANT: Colman, Steven

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Ellerman, Karen

; APPLICANT: Gerlach, Valerie

; APPLICANT: Gunther, Erik

; APPLICANT: Kekuda, Ramesh


```

; APPLICANT: MacDougall, John R.
; APPLICANT: Mehraban, Fuad
; APPLICANT: Patturajan, Meera
; APPLICANT: Rothenberg, Mark
; APPLICANT: Shimkets, Richard
; APPLICANT: Smithson, Glennnda
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Stone, David J.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
; TITLE OF INVENTION: USING THE SAME
; FILE REFERENCE: 21402-250 (CURA-550)
; CURRENT APPLICATION NUMBER: US/10/052,648A
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 60/262,454
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/272,920
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/284,549
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/303,229
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,605
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/269,098
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/264,159
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/271,855
; PRIOR FILING DATE: 2001-02-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 5000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-648A-7

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Query Match          18.6%;  Score 635.8;  DB 15;  Length 5000;
Best Local Similarity 57.3%;  Pred. No. 7.9e-195;
Matches 1232;  Conservative 0;  Mismatches 902;  Indels 15;  Gaps 4;

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Qy      62 GGACAGCATCACCTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTACT 121
      ||  ||  | |||| || |  || || ||  || ||  || || || || || || || ||
Db      129 GGCTGGCTGGAACCTCTCAACCCAGTGATCCCAATACCTGCAGCTTCTGGGAAAGCTTCA 188

Qy      122 CAGTGACTGTGCAAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGC- 180
      |  ||  | |||| || | | ||||  |  |  ||  |  || ||
Db      189 CTACCACCACCAAGGAGTCCCACTCCCGCCCTTCAGCCTGCTCCCTCAGAGCCCTGCG 248

Qy      181 --ACTGACATTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCT 238

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Db	249	AGCGGCCCTGGGAGGGCCCCATACTTGCCCCCAGCCCACGGTTGTATACCGGACCGTGT	308
Qy	239	ATCGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTGTCCTGGATTTTATG	298
Db	309	ACCGTCAGGTGGTGAAGACGGACCACCGCCAGCGCCTGCAGTGCTGCCATGGCTTCTATG	368
Qy	299	AAAGCGGGGAAATGTGTGTCCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTG	358
Db	369	AGAGCAGGGGGTTCTGTGTCCCGCTCTGTGCCCAGGAGTGTGTCCATGGCCGTTGTGTGG	428
Qy	359	CTCCAAACACCTGTCAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCG	418
Db	429	CACCCAATCAGTGCCAATGTGTGCCAGGCTGGCGGGGCGACGACTGTTCCAGTGAGTGTG	488
Qy	419	ATGGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGT	478
Db	489	CCCCAGGAATGTGGGGGCCACAGTGTGACAAGCCCTGCAGCTGCGGCAACAACAGCTCGT	548
Qy	479	GCAACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGG	538
Db	549	GTGATCCCAAGAGTGGGGTATGTTCTTGCCCTTCTGGTCTGCAGCCCCCGAAGTGCCTTC	608
Qy	539	ACCGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATG	598
Db	609	AGCCCTGTACCCCTGGCTACTATGGCCCTGCCTGCCAGTTCCGCTGCCAGTGCC---ATG	665
Qy	599	GAGCCACCTGCGACCACGTACGGGGGAATGCCGCTGCCCACCAGGATACACCGGAGCCT	658
Db	666	GGGCACCCTGCGATCCCCAGACTGGAGCCTGCTTCTGCCCCGCAGAGAGAACTGGGCCCA	725
Qy	659	TCTGTGAGGATCTTTGTCTCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTT	718
Db	726	GCTGTGACGTGTCTGTTCACAGGGCACTTCTGGCTTCTTCTGCCCCAGCACCCATCCTT	785
Qy	719	GTCAAATGGAGGAGTGTGTATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGA	778
Db	786	GCCAAAATGGAGGTGCTTCCAAACCCACAGGGCTCCTGCAGCTGCCCCCTGGCTGGA	845
Qy	779	TGGGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAG	838
Db	846	TGGGCACCATCTGCTCCCTGCCCTGCCAGAGGGCTTTCACGGACCCAATGCTCCCAGG	905
Qy	839	AATGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTC	898
Db	906	AATGTCGCTGCCACAACGGCGGCCTCTGTGACCGATTCACTGGGCAGTGCCGCTGCGCTC	965
Qy	899	CAGGATACACAGGGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCT	958
Db	966	CGGGTTACACTGGGGATCGGTGCCGGGAGGAGTGCCCGGTGGGCCGCTTTGGGCAGGACT	1025
Qy	959	GTGCTGAGACCTGCCAGTGTGTCAACGGAGGGAAGTGTACACGTGAGCGGCGCATGCC	1018
Db	1026	GTGCTGAGACGTGCGACTGCGCCCCGACGCCCCTTGCTTCCCGGCCAACGGCGCATGTC	1085
Qy	1019	TCTGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCCTGAGGGGCTCT	1078

Db 1086 TGTGCGAACACGGCTTCACTGGGGACCGCTGCACGGATCGCCTCTGCCCCGACGGCTTCT 1145
 Qy 1079 ACGGCATCAAATGTGACAAACGGTGTCCCTGCCACTTGGAAAACACTCATAGCTGTCACC 1138
 ||| ||| || | | | |||| || ||| ||| | |||| ||||
 Db 1146 ACGGTCTCAGCTGCCAGGCCCGCCGACCTGCGACCGGGAGCACAGCCTCAGCTGCCACC 1205
 Qy 1139 CCATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACAT 1198
 | ||| || ||||| ||||| ||||| ||| | ||| ||| ||| ||| |
 Db 1206 CGATGAACGGGGAGTGCTCCTGCCTGCCGGGCTGGGCGGGCCTCCACTGCAACGAGAGCT 1265
 Qy 1199 GTTCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAG 1258
 | | | | | ||| || ||||| || ||| ||||| | ||| |
 Db 1266 GCGCGCAGGACACGCATGGGCCAGGGTGCCAGGAGCACTGTCTCTGCCTGCACGGTGGCG 1325
 Qy 1259 ACTGTGACAGTGTGACTGGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCT 1318
 ||| | | | || || || || || || || || || || || || ||
 Db 1326 TCTGCCAGGCTACCAGCGGCCTCTGTCA GTGCGCGCCGGGTTACACGGGCCCTCACTGTG 1385
 Qy 1319 CTACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCCCTCTCGCTGTGGCTGTAAAA 1378
 ||| | || |||| | |||| || | ||||| || |||| || || ||
 Db 1386 CTAGTCTTTGTCTCCTGACACCTACGGTGTCAACTGTTCTGCACGCTGCTCATGTGAAA 1445
 Qy 1379 ATGATGCAGTCTGCTCTCCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCACGGGG 1438
 ||| | ||||| || | |||| || || ||||| || |||| | |
 Db 1446 ATGCCATCGCCTGCTCACCCATCGACGGCGAGTGCCTGCAAGGAAGGTTGGCAGCGTG 1505
 Qy 1439 TGGACTGCTCCATCAGATGTCCCAGTGGCACATGGGGCTTTGGCTGTAACCTAACATGCC 1498
 ||||| | || || || || || ||||| || || || || || ||
 Db 1506 GTAACCTGCTCTGTGCCCTGCCCACCGGAACCTGGGGCTTCAGTTGCAATGCCAGCTGCC 1565
 Qy 1499 AGTGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGAT 1558
 |||| | | || || || |||| || || || || || || || || || ||
 Db 1566 AGTGTGCCCATGAGGCAGTCTGCAGCCCCCAAACCTGGAGCCTGTACCTGCACCCCTGGGT 1625
 Qy 1559 GGCGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTG 1618
 ||| |||| | ||| | || |||| | | || || || || || || ||
 Db 1626 GGCATGGGGCCCACTGCCAGCTGCCCTGTCCGAAGGGGCAGTTTGAGAGAAGGTTGTGCCA 1685
 Qy 1619 AGCGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCC 1678
 |||| |||| |||| | ||||| |||| || || || || || || ||
 Db 1686 GTCGCTGTGACTGTGACCACTCTGATGGCTGTGACCCTGTTTCATGGACGCTGTCAGTGCC 1745
 Qy 1679 TCCCGGGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCA 1738
 | || ||| |||| || || || || || || || || || || || ||
 Db 1746 AGGCTGGCTGGATGGGTGCCCCGCTGCCACCTGTCCTGCCCTGAGGGCTTATGGGGAGTCA 1805
 Qy 1739 ACTGCTCCCTGCCCTGCTACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCT 1798
 |||| | |||| ||| || ||||| || || ||||| ||||| ||
 Db 1806 ACTGTAGCAACACCTGCACCTGCAAGAATGGGGGCACCTGTCTCCCTGAGAATGGCAACT 1865
 Qy 1799 GCGAGTGTGCACCAGGCTTCCGAGGCACCACTTGTGAGAGGATCTGCTCCCCTGGTTTTT 1858
 ||| ||||| || || ||||| ||| || || ||||| ||| ||||| |
 Db 1866 GCGTGTGTGCGCCCGGATTCCGGGGCCCCCTCCTGCCAGAGATCCTGTCAGCCTGGCCGCT 1925
 Qy 1859 ATGGGCATCGCTGCAGCCAGACATGCCACAGTGC GTTCACAGCAGCGGGCCCTGCCACC 1918
 |||| | |||| | | | |||| | || | | ||||| |||||
 Db 1926 ATGGCAAACGCTGTGTGC-----CCTGCAAGTGC GCTAACC ACTCC---TTCTGCCACC 1976

Qy 1919 ACATCACC GGCTGTGTGACTGCTTGCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGT 1978
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1977 CCTCGAACGGGACCTGCTACTGCCTGGCTGGCTGGACAGGCCCCGACTGCTCCCAGCCAT 2036
 Qy 1979 GTCCCAGTGGCAGATTTGGGAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAA 2038
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2037 GCCCTCCAGGACACTGGGGAGAAAACTGTGCCAGACCTGCCAATGTCACCATGGTGGGA 2096
 Qy 2039 CCTGTAACCCCATTTGACAGATCTTGTCAAGTGTACCCCGGTTGGATTGGCAGTGAAGTGT 2098
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2097 CCTGCCATCCCCAGGATGGGAGCTGTATCTGCCCCCTAGGCTGGACTGGACACCACTGCT 2156
 Qy 2099 CTCAACCATGTCCACCTGCCCACTGGGGCCCAAACCTGCATCCACACGTGCAACTGCCATA 2158
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2157 TAGAAGGCTGCCCTCTGGGGACATTTGGTGCTAACTGCTCCCAGCCATGCCAGTGTGGTC 2216
 Qy 2159 ATGGAGCTTTCTGCAGCGCCTACGATGGGGAATGTAAATGCACTCCTGG 2207
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 Db 2217 CTGGAGAAAAGTGCCACCCAGAGACTGGGGCCTGTGTATGTCCCCCAGG 2265

RESULT 8

US-09-796-753-99

; Sequence 99, Application US/09796753
 ; Publication No. US20030027998A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McCarthy, Sean A.
 ; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
 ; FILE REFERENCE: 7853-227-999
 ; CURRENT APPLICATION NUMBER: US/09/796,753
 ; CURRENT FILING DATE: 2001-03-01
 ; PRIOR APPLICATION NUMBER: 09/183,175
 ; PRIOR FILING DATE: 1998-10-30
 ; PRIOR APPLICATION NUMBER: 09/223,094
 ; PRIOR FILING DATE: 1998-12-30
 ; PRIOR APPLICATION NUMBER: 09/223,546
 ; PRIOR FILING DATE: 1998-12-30
 ; PRIOR APPLICATION NUMBER: 09/224,246
 ; PRIOR FILING DATE: 1998-12-30
 ; PRIOR APPLICATION NUMBER: 09/259,388
 ; PRIOR FILING DATE: 1999-02-26
 ; PRIOR APPLICATION NUMBER: 60/122,458
 ; PRIOR FILING DATE: 1999-03-01
 ; PRIOR APPLICATION NUMBER: 09/312,359
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: 09/336,536
 ; PRIOR FILING DATE: 1999-06-18
 ; PRIOR APPLICATION NUMBER: 09/342,687
 ; PRIOR FILING DATE: 1999-06-29
 ; PRIOR APPLICATION NUMBER: 09/345,464
 ; PRIOR FILING DATE: 1999-06-30
 ; PRIOR APPLICATION NUMBER: 09/365,164
 ; PRIOR FILING DATE: 1999-07-30
 ; PRIOR APPLICATION NUMBER: 09/399,723
 ; PRIOR FILING DATE: 1999-09-20
 ; PRIOR APPLICATION NUMBER: 09/409,634

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; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 99
; LENGTH: 3567
; TYPE: DNA
; ORGANISM: Rauttus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (925)...(2832)
US-09-796-753-99

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Query Match          17.8%; Score 608.4; DB 10; Length 3567;
Best Local Similarity 56.7%; Pred. No. 5.2e-186;
Matches 1226; Conservative 0; Mismatches 901; Indels 37; Gaps 4;

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Qy      67 GCATCACCTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTACTCAGTG 126
      ||  |  ||  ||  |  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      236 GCTGGAACACTCAACTCCAATGATCCCAATGTCTGTACCTTCTGGGAAAGCTTCACCACG 295

Qy      127 ACTGTGCAAGAGTCATACCCACATCCCTTT---GATCAAATTTACTACACGAGCTGCACT 183
      ||  |  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      296 ACCACTAAGGAGTCCCACCTTCGCCCCCTTCAGCCTGCCCCCAGCCGAGTCCTGCGACAGG 355

Qy      184 GACATTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCTATCGA 243
      |  |  ||  |  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      356 CCCTGGGAAGACCCCCACACCTGCGCTCAGCCTACGGTTGTCTACCGGACTGTGTACCGT 415

Qy      244 CATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTGTCTCGGATTTTATGAAAGC 303
      ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      416 CAGGTGGTGAAGATGGACTCCCGCCACGCCTGCAGTGCTGTGGGGGTTACTACGAGAGC 475

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Qy		304	GGGGAATGTGTGTCCTCCCACTGTGCTGATAAATGTGTCCATGGTTCGCTATTGCTCCA	363	
Db		476	AGTGGAGCCTGTGTCCCACACTCTGTGCCAGGAGTGTTGCCACGGTCGCTGTGTGGCTCCT	535	
Qy		364	AACACCTGTCAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGATGGT	423	
Db		536	AATCGGTGCCAGTGTGCACCAGGCTGGCGGGGTGACGACTGTTCCAGTGAGTGTGCTCCT	595	
Qy		424	GATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGCAAC	483	
Db		596	GGAATGTGGGGACCACAGTGTGACAGGCTCTGCCTCTGTGGCAACAGCAGTTCCTGTGAT	655	
Qy		484	CCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGACCGC	543	
Db		656	CCCAGGAGTGGGGTGTGTTTTTGGCCCTCTGGCCTGCAGCCCCCGACTGCCTTCAGCCT	715	
Qy		544	TGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATGGAGCC	603	
Db		716	TGCCCCGATGGCCACTATGGTCCTGCCTGCCAGTTTGATTGCCATTGC---TATGGGGCA	772	
Qy		604	ACCTGCGACCACGTACACGGGGGAATGCCGCTGCCACCAGGATACACCGGAGCCTTCTGT	663	
Db		773	TCCTGTGACCCCCGGGATGGAGCCTGCTTCTGCCCCCAGGGAGAACAGGACCCAGGGCA	832	
Qy		664	GAGGATCTTTGTCTCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGTCAA	723	
Db		833	CTGATGGCTTCTTCTGCCCCAGAAC-----TTATCCTTGCCAA	870	
Qy		724	AATGGAGGAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGATGGGC	783	
Db		871	AATGGAGGTGTTCTCAGGGCTCTCAAGGCTCCTGCAGCTGCCACCAGGGCTGGATGGGT	930	
Qy		784	ACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAATGC	843	
Db		931	GTCATCTGTTCCCTGCCATGCCAGAGGGTTTCCACGGACCCAACGTGACTCAGGAATGT	990	
Qy		844	CAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCAGGA	903	
Db		991	CGTTGCCACAATGGTGGCCTTTGTGACAGGTTTACTGGGCAGTGCCACTGTGCTCCTGGC	1050	
Qy		904	TACACAGGGGAACGGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTTCTCTGTGCT	963	
Db		1051	TATATCGGGGATCGGTGCCGTGAAGAGTGCCCTGTGGGCGCTTCGGTCAAGACTGTGCT	1110	
Qy		964	GAGACCTGCCAGTGTGTCAACGGAGGGAAGTGTTACCACGTGAGCGGCGCATGCCCTCTGT	1023	
Db		1111	GAGACCTGTGACTGTGCTCCTGGCGCTCGTTGCTTTTCTGCCAATGGCGCGTGTCTGTGC	1170	
Qy		1024	GAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCTGAGGGGCTCTACGGC	1083	
Db		1171	GAACATGGCTTCACAGGCGACCGCTGCACTGAGCGACTCTGTCCAGATGGCCGCTATGGT	1230	
Qy		1084	ATCAAATGTGACAAACGGTGTCCCTGCCACTTGAAAAACACTCATAGCTGTACCCCCATG	1143	
Db		1231	CTGAGCTGCCAAGATCCCTGCACCTGCGACCCAGAACACAGTCTCAGCTGCCACCCAATG	1290	
Qy		1144	TCTGGAGAGTGTGCTTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGTTCT	1203	

Db 1291 CACGGCGAGTGCTCCTGCCAGCCAGGTTGGGCGGGCCTCCACTGCAACGAGAGCTGCCCT 1350
 Qy 1204 CCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGT 1263
 Db 1351 CAGGACACGCACGGAGCCGGTTGCCAGGAGCACTGCCTCTGTCTGCACGGCGGTGTTTGC 1410
 Qy 1264 GACAGTGTGACTGGAAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACC 1323
 Db 1411 CTCGCCGACAGCGGCCTCTGCCGGTGTGCACCTGGCTACACGGGACCTCACTGCGCTAAT 1470
 Qy 1324 CCATGCCCTCTGGGAACCTATGGGATAAACTGTTCTCTCGCTGTGGCTGTAAAAATGAT 1383
 Db 1471 CTTTGTCCACCTAACACTTATGGGATCAACTGTTCTCCCACTGCTCCTGTGAAAATGCC 1530
 Qy 1384 GCAGTCTGCTCTCCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCAGGGGTGGAC 1443
 Db 1531 ATTGCCCTGCTCTCCTGTGACGGCACGTGCATCTGCAAGGAAGTTGGCAGCGTGGTAAC 1590
 Qy 1444 TGCTCCATCAGATGTCCCAGTGGCACATGGGGCTTTGGCTGTAACCTAACATGCCAGTGC 1503
 Db 1591 TGCTCTGTGCCCTGTCCCCCTGGCACCTGGGGCTTCAGTTGCAATGCCAGTTGCCAGTGT 1650
 Qy 1504 CTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGGCGC 1563
 Db 1651 GCCACGAGGGAGTCTGCAGCCCCCAAACCTGGAGCCTGTACTTGACCCCTGGGTGGCGT 1710
 Qy 1564 GGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAGCGC 1623
 Db 1711 GGGGTTCACTGCCAACTTCCGTGCCCCAAGGGACAGTTTGGTGAAGGTTGTGCCAGTGTG 1770
 Qy 1624 TGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTCCCG 1683
 Db 1771 TGTGACTGTGACCACTCCGATGGCTGTGACCCTGTTTCATGGACACTGCCGATGTCAGGCT 1830
 Qy 1684 GGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAACTGC 1743
 Db 1831 GGCTGGATGGGCACACGTTGCCACCTGCCTTGCCCAGAGGGCTTTTGGGGAGCCAACTGC 1890
 Qy 1744 TCCCTGCCCTGCTACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGCGAG 1803
 Db 1891 AGCAATGCCTGTACCTGCAAGAATGGTGGCACTTGTGTACCTGAGAACGGCAACTGTGTG 1950
 Qy 1804 TGTGCACCAGGCTTCCGAGGCACCACTTGTGAGAGGATCTGCTCCCCTGGTTTTTATGGG 1863
 Db 1951 TGCGCACCAGGGTTCAGAGGCCCTCCTGCCAGAGGCCCTGCCCGCTGGTTCGCTATGGC 2010
 Qy 1864 CATCGCTGCAGCCAGACATGCCCACAGTGCCTTCACAGCAGCGGGCCCTGCCACCACATC 1923
 Db 2011 AAACGCTG-----TGTGCCCTGCAAGTGCAACAACCATTCTTCCTGCCACCCGTCG 2061
 Qy 1924 ACCGGCCTGTGTGACTGCTTGCCCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGTCC 1983
 Db 2062 GATGGGACCTGCTCCTGCCTGGCAGGCTGGACAGGCCCTGACTGCTCTGAATCATGTCCC 2121
 Qy 1984 AGTGGCAGATTTGGGAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACCTGT 2043

Db 2122 CCAGGCCACTGGGGACTCAAATGCTCCCAACCCTGCCAGTGTTCATCATGGTGCCACCTGC 2181
 Qy 2044 AACCCCATTTGACAGATCTTGTCTAGTGTTACCCCGGTTGGATTGGCAGTGACTGCTCTCAA 2103
 ||||| || | ||| || ||| || ||| ||| ||||| ||
 Db 2182 CACCCCCAGGATGGGAGCTGTGTCTGCATCCCAGGCTGGACTGGACCCAAGTCTCGGAA 2241
 Qy 2104 CCATGTCCACCTGCCCCACTGGGGCCCAAAGTGCATCCACACGTGCAACTGCCATAATGGA 2163
 || ||| | | || ||||| || | || || ||||
 Db 2242 GGCTGCCCATCAAGAATGTTTGGTGTCAACTGCTCCCAGCTATGTCAGTGTGATCCTGGA 2301
 Qy 2164 GCTTTCTGCAGCGCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTCTAC 2223
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 Db 2302 GAGATGTGCCACCCAGAGACTGGGGCTTGCCTGTGTCCCCCAGGACACAGTGGTGCGCAC 2361
 Qy 2224 TGCA 2227
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 Db 2362 TGCA 2365

RESULT 9

US-09-796-753-123

; Sequence 123, Application US/09796753

; Publication No. US20030027998A1

; GENERAL INFORMATION:

; APPLICANT: McCarthy, Sean A.

; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

; FILE REFERENCE: 7853-227-999

; CURRENT APPLICATION NUMBER: US/09/796,753

; CURRENT FILING DATE: 2001-03-01

; PRIOR APPLICATION NUMBER: 09/183,175

; PRIOR FILING DATE: 1998-10-30

; PRIOR APPLICATION NUMBER: 09/223,094

; PRIOR FILING DATE: 1998-12-30

; PRIOR APPLICATION NUMBER: 09/223,546

; PRIOR FILING DATE: 1998-12-30

; PRIOR APPLICATION NUMBER: 09/224,246

; PRIOR FILING DATE: 1998-12-30

; PRIOR APPLICATION NUMBER: 09/259,388

; PRIOR FILING DATE: 1999-02-26

; PRIOR APPLICATION NUMBER: 60/122,458

; PRIOR FILING DATE: 1999-03-01

; PRIOR APPLICATION NUMBER: 09/312,359

; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: 09/336,536

; PRIOR FILING DATE: 1999-06-18

; PRIOR APPLICATION NUMBER: 09/342,687

; PRIOR FILING DATE: 1999-06-29

; PRIOR APPLICATION NUMBER: 09/345,464

; PRIOR FILING DATE: 1999-06-30

; PRIOR APPLICATION NUMBER: 09/365,164

; PRIOR FILING DATE: 1999-07-30

; PRIOR APPLICATION NUMBER: 09/399,723

; PRIOR FILING DATE: 1999-09-20

; PRIOR APPLICATION NUMBER: 09/409,634

; PRIOR FILING DATE: 1999-09-30

; PRIOR APPLICATION NUMBER: 09/471,179

; PRIOR FILING DATE: 1999-12-23


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; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
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; PRIOR FILING DATE: 2000-05-14
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; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 123
; LENGTH: 3567
; TYPE: DNA
; ORGANISM: Rauttus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (925)...(2832)
US-09-796-753-123

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Query Match          17.8%; Score 608.4; DB 10; Length 3567;
Best Local Similarity 56.7%; Pred. No. 5.2e-186;
Matches 1226; Conservative 0; Mismatches 901; Indels 37; Gaps 4;

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Qy      67 GCATCACCTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTACTCAGTG 126
      ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      236 GCTGGAACACTCAACTCCAATGATCCCAATGTCTGTACCTTCTGGGAAAGCTTCACCACG 295

Qy      127 ACTGTGCAAGAGTCATACCCACATCCCTTT---GATCAAATTTACTACACGAGCTGCACT 183
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Db      296 ACCACTAAGGAGTCCCACCTTCGCCCCCTTCAGCCTGCCCCAGCCGAGTCCTGCGACAGG 355

Qy      184 GACATTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCTATCGA 243
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      356 CCCTGGGAAGACCCCCACACCTGCGCTCAGCCTACGGTTGTCTACCGGACTGTGTACCGT 415

Qy      244 CATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTGTCCTGGATTTTATGAAAGC 303
      ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      416 CAGGTGGTGAAGATGGACTCCCGCCACGCCTGCAGTGCTGTGGGGTTACTACGAGAGC 475

Qy      304 GGGGAAATGTGTGTCCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTGCTCCA 363
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      476 AGTGGAGCCTGTGTCCCACTCTGTGCCCAGGAGTGTGTCCACGGTCGCTGTGTGGCTCCT 535

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Qy 364 AACACCTGTCAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCGATGGT 423
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 Db 536 AATCGGTGCCAGTGTGCACCAGGCTGGCGGGGTGACGACTGTTCAGTGAGTGTGCTCCT 595
 Qy 424 GATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGTGCAAC 483
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 Db 596 GGAATGTGGGGACCACAGTGTGACAGGCTCTGCCTCTGTGGCAACAGCAGTTCCTGTGAT 655
 Qy 484 CCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGGACCGC 543
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 Db 656 CCCAGGAGTGGGGTGTGTTTTGCCCTCTGGCCTGCAGCCCCCGACTGCCTTCAGCCT 715
 Qy 544 TGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATGGAGCC 603
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 Db 716 TGCCCCGATGGCCACTATGGTCCTGCCTGCCAGTTTGATTGCCATTGC---TATGGGGCA 772
 Qy 604 ACCTGCGACCACGTACGCGGGGAATGCCGCTGCCACCAGGATACACCGGAGCCTTCTGT 663
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 Db 773 TCCTGTGACCCCCGGGATGGAGCCTGCTTCTGCCCCCAGGGAGAACAGGACCCAGGGCA 832
 Qy 664 GAGGATCTTTGTCTCTGTTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTTGTCAA 723
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 Db 833 CTGATGGCTTCTTCTGCCCCAGAAC-----TTATCCTTGCCAA 870
 Qy 724 AATGGAGGAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGATGGGC 783
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 Db 871 AATGGAGGTGTTTCTCAGGGCTCTCAAGGCTCCTGCAGCTGCCACCGGGCTGGATGGGT 930
 Qy 784 ACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTGTTCCCAAGAATGC 843
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 Db 931 GTCATCTGTTCCCTGCCATGCCAGAGGGTTTCCACGGACCCAACTGTACTCAGGAATGT 990
 Qy 844 CAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCATTGCAGTCCAGGA 903
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 Db 991 CGTTGCCACAATGGTGGCCTTTGTGACAGGTTTACTGGGCAGTGCCACTGTGCTCCTGGC 1050
 Qy 904 TACACAGGGGAACGGTGCCAGGATGAGTGTCTGTGGGACCTATGGCGTTCTCTGTGCT 963
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 Db 1051 TATATCGGGGATCGGTGCCGTGAAGAGTGCCTGTGGGCCGCTTCGGTCAAGACTGTGCT 1110
 Qy 964 GAGACCTGCCAGTGTGTCAACGGAGGGAAGTGTACCACGTGAGCGGCGCATGCCTCTGT 1023
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 Db 1111 GAGACCTGTGACTGTGCTCCTGGCGCTCGTTGCTTTCCTGCCAATGGCGCGTGTCTGTGC 1170
 Qy 1024 GAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCCTGAGGGGCTCTACGGC 1083
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 Db 1171 GAACATGGCTTCACAGGCGACCGCTGCACTGAGCGACTCTGTCCAGATGGCCGCTATGGT 1230
 Qy 1084 ATCAAATGTGACAAACGGTGTCCCTGCCACTTGGAACAACTCATAGCTGTACCCCATG 1143
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 Db 1231 CTGAGCTGCCAAGATCCCTGCACCTGCGACCCAGAACACAGTCTCAGCTGCCACCCAATG 1290
 Qy 1144 TCTGGAGAGTGTGCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGTTCT 1203
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 Db 1291 CACGGCGAGTGCTCCTGCCAGCCAGGTTGGGCGGGCCTCCACTGCAACGAGAGCTGCCCT 1350

Qy 1204 CCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGT 1263
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 Db 1351 CAGGACACGCACGGAGCCGGTTGCCAGGAGCACTGCCTCTGTCTGCACGGCGGTGTTTGC 1410

Qy 1264 GACAGTGTGACTGGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACC 1323
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 Db 1411 CTCGCCGACACGGCCTCTGCCGGTGTGCACCTGGCTACACGGGACCTCACTGCGCTAAT 1470

Qy 1324 CCATGCCCTCTGGGAACCTATGGGATAAACTGTTCCCTCTCGCTGTGGCTGTAAAAATGAT 1383
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 Db 1471 CTTTGTCCACCTAACACTTATGGGATCAACTGTTCCCTCCCACTGCTCCTGTGAAAATGCC 1530

Qy 1384 GCAGTCTGCTCTCCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTGGCACGGGGTGGAC 1443
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 Db 1531 ATTGCCTGCTCTCCTGTGACGGCACGTGCATCTGCAAGGAAGGTTGGCAGCGTGGTAAC 1590

Qy 1444 TGCTCCATCAGATGTCCCAGTGGCACATGGGGCTTTGGCTGTAACCTAACATGCCAGTGC 1503
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 Db 1591 TGCTCTGTGCCCTGTCCCCCTGGCACCTGGGGCTTCAGTTGCAATGCCAGTTGCCAGTGT 1650

Qy 1504 CTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGCACCTGGATGGCGC 1563
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 Db 1651 GCCCACGAGGGAGTCTGCAGCCCCCAAACCTGGAGCCTGTACTTGCACCCCTGGGTGGCGT 1710

Qy 1564 GGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAACTGTGCTGAGCGC 1623
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 Db 1711 GGGGTTCACTGCCAACTTCCGTGCCCCGAAGGGACAGTTTGGTGAAGGTTGTGCCAGTGT 1770

Qy 1624 TGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTGCCGCTGCCTCCCG 1683
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 Db 1771 TGTGACTGTGACCACTCCGATGGCTGTGACCCTGTTTCATGGACACTGCCGATGTCAGGCT 1830

Qy 1684 GGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTGGGGCCCCAACTGC 1743
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 Db 1831 GGCTGGATGGGCACACGTTGCCACCTGCCTTGCCAGAGGGCTTTTGGGGAGCCAACCTGC 1890

Qy 1744 TCCCTGCCCTGCTACTGTAAAAATGGGGCTTCATGCTCCCCTGATGATGGCATCTGCGAG 1803
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 Db 1891 AGCAATGCCTGTACCTGCAAGAATGGTGGCACTTGTGTACCTGAGAACGGCAACTGTGTG 1950

Qy 1804 TGTGCACCAGGCTTCCGAGGCACCACTTGTGAGAGGATCTGCTCCCCTGGTTTTTATGGG 1863
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1951 TGCGCACCAGGGTTCAGAGGCCCTCCTGCCAGAGGCCCTGCCCGCTGGTTCGCTATGGC 2010

Qy 1864 CATCGCTGCAGCCAGACATGCCACAGTGCCTTACAGCAGCGGGCCCTGCCACCACATC 1923
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 Db 2011 AAACGCTG-----TGTGCCCTGCAAGTGCAACAACCATTCTTCCTGCCACCCGTCG 2061

Qy 1924 ACCGGCCTGTGTGACTGCTTGCTGGCTTCACAGGCGCCCTCTGCAATGAAGTGTGTCCC 1983
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 Db 2062 GATGGGACCTGCTCCTGCCTGGCAGGCTGGACAGGCCCTGACTGCTCTGAATCATGTCCC 2121

Qy 1984 AGTGGCAGATTTGGGAAAACTGTGCAGGAATTTGTACCTGCACCAACAACGGAACCTGT 2043
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 Db 2122 CCAGGCCACTGGGGACTCAAATGCTCCCAACCCTGCCAGTGTGCATCATGGTGCCACCTGC 2181

Qy 2044 AACCCCATTGACAGATCTTGTGAGTGTACCCCGGTTGGATTGGCAGTGACTGCTCTCAA 2103

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Db      2182 CACCCCCAGGATGGGAGCTGTGTCTGCATCCCAGGCTGGACTGGACCCAAGTCTCGGAA 2241

Qy      2104 CCATGTCCACCTGCCCCTGGGGCCCAAAGTGCATCCACACGTGCAACTGCCATAATGGA 2163
      || ||| |  | ||  ||||| |||  ||  || || || |||
Db      2242 GGCTGCCCATCAAGAATGTTTGGTGTCAACTGCTCCCAGCTATGTCAGTGTGATCCTGGA 2301

Qy      2164 GCTTTCTGCAGCGCCTACGATGGGGAATGTAAATGCACTCCTGGCTGGACAGGGCTCTAC 2223
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Db      2302 GAGATGTGCCACCCAGAGACTGGGGCTTGCGTCTGTCCCCCAGGACACAGTGGTGCAC 2361

Qy      2224 TGCA 2227
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Db      2362 TGCA 2365

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RESULT 10

US-10-052-648A-3

; Sequence 3, Application US/10052648A

; Publication No. US20040005558A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, David

; APPLICANT: Burgess, Catherine

; APPLICANT: Casman, Stacie

; APPLICANT: Colman, Steven

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Ellerman, Karen

; APPLICANT: Gerlach, Valerie

; APPLICANT: Gunther, Erik

; APPLICANT: Kekuda, Ramesh

; APPLICANT: MacDougall, John R.

; APPLICANT: Mehraban, Fuad

; APPLICANT: Patturajan, Meera

; APPLICANT: Rothenberg, Mark

; APPLICANT: Shimkets, Richard

; APPLICANT: Smithson, Glennnda

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Stone, David J.

; APPLICANT: Vernet, Corine A.M.

; APPLICANT: Zerhusen, Bryan D.

; TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF

; TITLE OF INVENTION: USING THE SAME

; FILE REFERENCE: 21402-250 (CURA-550)

; CURRENT APPLICATION NUMBER: US/10/052,648A

; CURRENT FILING DATE: 2002-12-09

; PRIOR APPLICATION NUMBER: 60/262,454

; PRIOR FILING DATE: 2001-01-18

; PRIOR APPLICATION NUMBER: 60/272,920

; PRIOR FILING DATE: 2001-03-02

; PRIOR APPLICATION NUMBER: 60/284,549

; PRIOR FILING DATE: 2001-04-18

; PRIOR APPLICATION NUMBER: 60/303,229

; PRIOR FILING DATE: 2001-07-05

; PRIOR APPLICATION NUMBER: 60/262,892

; PRIOR FILING DATE: 2001-01-19

; PRIOR APPLICATION NUMBER: 60/263,605

; PRIOR FILING DATE: 2001-01-23

```
; PRIOR APPLICATION NUMBER: 60/269,098
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/264,159
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/271,855
; PRIOR FILING DATE: 2001-02-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 2919
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-052-648A-3
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Qy	62	GGACAGCATCACCTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTACT	121
Db	129	GGCTGGCTGGAACCTCTCAACCCCAGTGATCCCAATACCTGCAGCTTCTGGGAAAGCTTCA	188
Qy	122	CAGTGACTGTGCAAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGC-	180
Db	189	CTACCACCACCAAGGAGTCCCCTCCCGCCCCTTCAGCCTGCTCCCCTCAGAGCCCTGCG	248
Qy	181	--ACTGACATTTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCT	238
Db	249	AGCGGCCCTGGGAGGGCCCCCATACTTGCCCCCAGCCACGTTGTATACCGGACCGTGT	308
Qy	239	ATCGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTGTGCTCGGATTTTATG	298
Db	309	ACCGTCAGTGGTGAAGACGGACCACCGCCAGCGCCTGCAGTGTGCCATGGCTTCTATG	368
Qy	299	AAAGCGGGGAAATGTGTGTCCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTG	358
Db	369	AGAGCAGGGGGTTCTGTGTCCCGCTCTGTGCCCAGGAGTGTGTCCATGGCCGTTGTGTGG	428
Qy	359	CTCCAAACACCTGTCTAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCG	418
Db	429	CACCCAATCAGTGCCAAATGTGTGCCAGGCTGGCGGGGCGACGACTGTTCCAGTGAGTGTG	488
Qy	419	ATGGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGT	478
Db	489	CCCCAGGAATGTGGGGGCCACAGTGTGACAAGCCCTGCAGCTGCGGCAACAACAGCTCGT	548
Qy	479	GCAACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGG	538
Db	549	GTGATCCCAAGAGTGGGGTATGTTCTTGCCCTTCTGGTCTGCAGCCCCGAAGTGCCTTC	608
Qy	539	ACCGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATG	598
Db	609	AGCCCTGTACCCCTGGCTACTATGGCCCTGCCTGCCAGTTCGCTGCCAGTGCC---ATG	665

Qy 599 GAGCCACCTGCGACCACGTACGCGGGGAATGCCGCTGCCACACAGGATACACCGGAGCCT 658
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 Db 666 GGGCACCTGCGATCCCCAGACTGGAGCCTGCTTCTGCCCCGCAGAGAGAACTGGGCCCA 725

 Qy 659 TCTGTGAGGATCTTTGTCCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTT 718
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 Db 726 GCTGTGACGTGTCTGTTCACAGGGCACTTCTGGCTTCTTCTGCCCCAGCACCCATTCTT 785

 Qy 719 GTCAAATGGAGGAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGA 778
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 Db 786 GCCAAATGGAGGTGTCTTCCAAACCCACAGGGCTCCTGCAGCTGCCCCCTGGCTGGA 845

 Qy 779 T----- 779
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 Db 846 TGGTATGGAGGTGGGGCCTGTGGGCATGGGGTGTGGGTCTGGGGAGAATTCTGTGGGTG 905

 Qy 780 -----GGGCACAGTGTGTGGTTCAGCCTTGCCCCGAGGGTCGCTTTG 820
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 Db 906 GTGCTAAGCAGGGCTCCAAGGGCACCATCTGCTCCCTGCCCTGCCAGAGGGCTTTCACG 965

 Qy 821 GAAAGAACTGTTCCCAAGAATGCCAGTGCATAATGGAGGGACGTGTGATGCTGCCACAG 880
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 Db 966 GACCCAAGTGTCTCCAGGAATGTCGCTGCCACAACGGCGGCCTCTGTGACCGATTCACTG 1025

 Qy 881 GCCAATGTCATTGCAGTCCAGGATACACAGGGGAACGGTGCCAGGATGAGTGTCTGTG 940
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 Db 1026 GGCAGTGCCGCTGCGCTCCGGGTACACTGGGGATCGGTGCCGGGAGGAGTGCCCGGTGG 1085

 Qy 941 GGACCTATGGCGTTCTCTGTGCTGAGACCTGCCAGTGTGTCAACGGAGGGAAGTGTACC 1000
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 Db 1086 GCCGCTTTGGGCAGGACTGTGCTGAGACGTGCGACTGCGCCCCGGACGCCCGTTGCTTCC 1145

 Qy 1001 ACGTGAGCGGCGCATGCCTCTGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCC 1060
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 Db 1146 CGGCCAACGGCGCATGTCTGTGCGAACACGGCTTCACTGGGGACCGCTGCACGGATCGCC 1205

 Qy 1061 TGTGTCCTGAGGGGCTCTACGGCATCAAATGTGACAAACGGTGTCCCTGCCACTTGAAA 1120
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 Db 1206 TCTGCCCCGACGGCTTCTACGGTCTCAGCTGCCAGGCCCCCGCACCTGCGACCGGGAGC 1265

 Qy 1121 AACTCATAGCTGTCACCCCATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGAC 1180
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 Db 1266 ACAGCCTCAGCTGCCACCCGATGAACGGGGAGTGTCTCCTGCCTGCCGGGCTGGCGGGCC 1325

 Qy 1181 TCTACTGTAATGAGACATGTTCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCA 1240
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 Db 1326 TCCACTGCAACGAGAGCTGCCCGCAGGACACGCATGGGCCAGGGTGCCAGGAGCACTGTC 1385

 Qy 1241 GCTGCCAAATGGGGCAGACTGTGACAGTGTGACTGGAAAGTGACCTGTGCCCCAGGAT 1300
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 Db 1386 TCTGCCTGCACGGTGGCGTCTGCCAGGCTACCAGCGCCTCTGTGAGTGCAGCGCGGGTT 1445

 Qy 1301 TCAAAGGAATTGACTGCTCTACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCTT 1360
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 Db 1446 ACACGGGCCCTCACTGTGCTAGTCTTTGTCTCCTGACACCTACGGTGTCAACTGTTCTG 1505

 Qy 1361 CTCGCTGTGGCTGTAAAAATGATGCAGTCTGCTCTCCTGTGGACGGGTCTTGTACTTGCA 1420

Db	1506	CACGCTGCTCATGTGAAAAATGCCATCGCCTGCTCACCCATCGACGGCGAGTGCCTCTGCA	1565
Qy	1421	AGGCAGGCTGGCACGGGGTGGACTGCTCCATCAGATGTCCCAGTGGCACATGGGGCTTTG	1480
Db	1566	AGGAAGGTTGGCAGCGTGGTAACTGCTCTGTGCCCTGCCCACCCGGAACCTGGGGCTTCA	1625
Qy	1481	GCTGTAACCTTAACATGCCAGTGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCT	1540
Db	1626	GTTGCAATGCCAGCTGCCAGTGTGCCCATGAGGCAGTCTGCAGCCCCCAAACCTGGAGCCCT	1685
Qy	1541	GCACGTGTGCACCTGGATGGCGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGT	1600
Db	1686	GTACCTGCACCCCTGGGTGGCATGGGGCCCACTGCCAGCTGCCCTGTCCGAAGGGGCAGT	1745
Qy	1601	ACGGGCTGAACTGTGCTGAGCGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCA	1660
Db	1746	TTGGAGAAGGTTGTGCCAGTCGCTGTGACTGTGACCACTCTGATGGCTGTGACCCTGTTC	1805
Qy	1661	CGGGCCATTGCCGCTGCCTCCCGGGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTG	1720
Db	1806	ATGGACGCTGTCAGTGCCAGGCTGGCTGGATGGGTGCCCGCTGCCACCTGTCCTGCCCTG	1865
Qy	1721	AGGGACGCTGGGGCCCCAACTGCTCCCTGCCCTGCTACTGTAAAAATGGGGCTTCATGCT	1780
Db	1866	AGGGCTTATGGGGAGTCAACTGTAGCAACACCTGCACCTGCAAGAATGGGGGCACCTGTC	1925
Qy	1781	CCCCTGATGATGGCATCTGCGAGTGTGCACCAGGCTTCCGAGGCACCACTTGTGAGAGGA	1840
Db	1926	TCCCTGAGAATGGCAACTGCGTGTGTGCGCCCGGATTCCGGGGCCCCCTCCTGCCAGAGAT	1985
Qy	1841	TCTGCTCCCCTGGTTTTTATGGGCATCGCTGCAGCCAGACATGCCCACAGTGCCTTCACA	1900
Db	1986	CCTGTCAGCCTGGCCGCTATGGCAAACGCTGTGTGC-----CCTGCAAGTGCCTAACC	2039
Qy	1901	GCAGCGGGCCCTGCCACCACATCACGGCCCTGTGTGACTGCTTGCCTGGCTTCACAGGCG	1960
Db	2040	ACTCC---TTCTGCCACCCCTCGAACGGGGCCTGCTACTGCCTGGCTGGCTGGACAGGCC	2096
Qy	1961	CCCTCTGCAATGAAGTGTGTCCAGTGGCAGATTTGGGAAAAACTGTGCAGGAATTTGTA	2020
Db	2097	CCGACTGCTCCCAGCCATGCCCTCCAGGACACTGGGGAGAAAACTGTGCCAGACCTGCC	2156
Qy	2021	CCTGCACCAACAACGGAACCTGTAACCCCATTGACAGATCTTGTGAGTGTACCCCGGTT	2080
Db	2157	AATGTCACCATGGTGGGACCTGCCATCCCAGGATGGGAGCTGTATCTGCCCCCTAGGCT	2216
Qy	2081	GGATTGGCAGTGACTGCTCTCAACCATGTCCACCTGCCCCTGGGGCCCCAACTGCATCC	2140
Db	2217	GGACTGGACACCACTGCTTAGAAGGCTGCCCTCTGGGGACATTTGGTGCTAACTGCTCCC	2276
Qy	2141	ACACGTGCAACTGCCATAATGGAGCTTTCTGCAGCGCCTACGATGGGGAATGTAAATGCA	2200
Db	2277	AGCCATGCCAGTGTGGTCCTGGAGAAAAGTGCCACCCAGAGACTGGGGCCTGTGTATGTC	2336
Qy	2201	CTCCTGG 2207	

Db 2337 CCCCAGG 2343

RESULT 11

US-10-052-648A-5

; Sequence 5, Application US/10052648A
; Publication No. US20040005558A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Colman, Steven
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gunther, Erik
; APPLICANT: Kekuda, Ramesh
; APPLICANT: MacDougall, John R.
; APPLICANT: Mehraban, Fuad
; APPLICANT: Patturajan, Meera
; APPLICANT: Rothenberg, Mark
; APPLICANT: Shimkets, Richard
; APPLICANT: Smithson, Glennda
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Stone, David J.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
; TITLE OF INVENTION: USING THE SAME
; FILE REFERENCE: 21402-250 (CURA-550)
; CURRENT APPLICATION NUMBER: US/10/052,648A
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 60/262,454
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/272,920
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/284,549
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/303,229
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; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,605
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/269,098
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/264,159
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/271,855
; PRIOR FILING DATE: 2001-02-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2919

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-648A-5

Query Match 16.0%; Score 546.2; DB 15; Length 2919;
Best Local Similarity 55.3%; Pred. No. 8e-166;
Matches 1231; Conservative 0; Mismatches 903; Indels 93; Gaps 5;

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Qy      62 GGACAGCATCACCTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTACT 121
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Db      129 GGCTGGCTGGAACCTCTCAACCCAGTGATCCCAATACCTGCAGCTTCTGGGAAAGCTTCA 188

Qy      122 CAGTGACTGTGCAAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGC- 180
      |  ||  | ||| ||  ||  || || ||  |  |  ||  |  |||
Db      189 CTACCACCACCAAGGAGTCCCACTCCCGCCCTTCAGCCTGCTCCCTCAGAGCCCTGCG 248

Qy      181 --ACTGACATTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCT 238
      |  |  |  ||  ||  || || || ||  ||  || || || ||  |  |
Db      249 AGCGGCCCTGGGAGGGCCCCCATACTTGCCCCAGCCCACGGTTGTATACGGACCGTGT 308

Qy      239 ATCGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTGTCTGGATTTTATG 298
      | || || | || |||||  |  |  |  |||| || | ||| || |||
Db      309 ACCGTGAGGTGGTGAAGACGGACCACCGCCAGCGCCTGCAGTGCTGCCATGGCTTCTATG 368

Qy      299 AAAGCGGGGAAATGTGTGTCCCCCACTGTGCTGATAAATGTGTCCATGGTCGCTGTATTG 358
      | ||| |||  | ||||| ||  |||||  |  | ||||| |||| || ||| |
Db      369 AGAGCAGGGGTTCTGTGTCCCGCTCTGTGCCAGGAGTGTGTCCATGGCCGTTGTGTGG 428

Qy      359 CTCCAAACACCTGTCAGTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCG 418
      | || ||  || || ||| || ||||| ||  || || ||||| |||| || |
Db      429 CACCAATCAGTGCCAATGTGTGCCAGGCTGGCGGGGCGACGACTGTTCCAGTGAGTGTG 488

Qy      419 ATGGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGT 478
      |  |||| || || ||  ||  | |||  |||  ||  ||
Db      489 CCCCAGGAATGTGGGGGCCACAGTGTGACAAGCCCTGCAGCTGCGGCAACAACAGCTCGT 548

Qy      479 GCAACCCCATCACCGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGG 538
      |  ||||  | ||||  ||  || || || ||  |  |  |||
Db      549 GTGATCCCAAGAGTGGGGTATGTTCTTGCCCTTCTGGTCTGCAGCCCCGAAGTGCCTTC 608

Qy      539 ACCGCTGTGAGCAGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATG 598
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Db      609 AGCCCTGTACCCCTGGCTACTATGGCCCTGCCTGCCAGTTCGGCTGCCAGTGCC---ATG 665

Qy      599 GAGCCACCTGCGACCACGTACGCGGGAATGCCGCTGCCACCAGGATACACCGGAGCCT 658
      | ||  ||||| ||  || || || || || ||||| |||  || || ||
Db      666 GGGCACCTGCGATCCCCAGACTGGAGCCTGCTTCTGCCCCGAGAGAGAACTGGGCCCA 725

Qy      659 TCTGTGAGGATCTTTGTCTCTCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTT 718
      ||||| |  ||| | | ||  |||  ||  ||  |  |||
Db      726 GCTGTGACGTGTCCTGTTCCAGGGCACTTCTGGCTTCTTCTGCCCCAGCACCCATTCTT 785

Qy      719 GTCAAAATGGAGGAGTGTGTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGA 778
      | ||||| |||| || | ||  |  ||  |||  ||||  ||||| |||
Db      786 GCCAAAATGGAGGTGTCTTCCAAACCCACAGGGCTCCTGCAGCTGCCCCCTGGCTGGA 845

Qy      779 T----- 779
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Db	846	TGGTATGGAGGGTGGGGCCTGTGGGCATGGGGTGTGGGTCTGGGGAGAATTCTGTGGGTG	905
Qy	780	-----GGGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTG	820
Db	906	GTGCTAAGCAGGGCTCCAAGGGCACCATCTGCTCCCTGCCCTGCCAGAGGGCTTTCACG	965
Qy	821	GAAAGAACTGTTCCCAAGAATGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAG	880
Db	966	GACCCAACTGCTCCCAGGAATGTGCTGCCACAACGGCGGCCTCTGTGACCGATTCACTG	1025
Qy	881	GCCAATGTCATTGCAGTCCAGGATACACAGGGGAACGGTGCCAGGATGAGTGTCTGTG	940
Db	1026	GGCAGTGCCGCTGCGCTCCGGGTTACACTGGGGATCGGTGCCGGGAGGAGTGCCCGGTG	1085
Qy	941	GGACCTATGGCGTTCTCTGTGCTGAGACCTGCCAGTGTGTCAACGGAGGGAAGTGTTACC	1000
Db	1086	GCCGCTTTGGGCAGGACTGTGCTGAGACGTGCGACTGCGCCCCGGACGCCCGTTGCTTCC	1145
Qy	1001	ACGTGAGCGGCGCATGCCTCTGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCC	1060
Db	1146	CGGCCAACGGCGCATGTCTGTGCGAACACGGCTTCACTGGGGACCGCTGCACGGATCGCC	1205
Qy	1061	TGTGTCCTGAGGGGCTCTACGGCATCAAATGTGACAAACGGTGTCCCTGCCACTTGGAAA	1120
Db	1206	TCTGCCCCGACGGCTTCTACGGTCTCAGCTGCCAGGCCCGCCGACCTGCGACCGGGAGC	1265
Qy	1121	ACACTCATAGCTGTCACCCCATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGAC	1180
Db	1266	ACAGCCTCAGCTGCCACCCGATGAACGGGGAGTGCTCCTGCCCTGCCGGGCTGGGCGGGCC	1325
Qy	1181	TCTACTGTAATGAGACATGTTCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCA	1240
Db	1326	TCCACTGCAACGAGAGCTGCCCCGAGGACACGCATGGGCCAGGGTGCCAGGAGCGCTGTC	1385
Qy	1241	GCTGCCAAAATGGGGCAGACTGTGACAGTGTGACTGGAAAGTGACCTGTGCCCCAGGAT	1300
Db	1386	TCTGCCTGCACGGTGGCGTCTGCCAGGCTACCAGCGGCCTCTGTCAGTGCGCGCCGGGTT	1445
Qy	1301	TCAAAGGAATTGACTGCTCTACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCCCT	1360
Db	1446	ACACGGGCCCTCACTGTGCTAGTCTTTGTCTCCTGACACCTACGGTGTCAACTGTTCTG	1505
Qy	1361	CTCGCTGTGGCTGTAAAAATGATGCAGTCTGCTCTCCTGTGGACGGGTCTTGTACTTGCA	1420
Db	1506	CACGCTGCTCATGTGAAAATGCCATCGCCTGCTCACCCATCGACGGCGAGTGCGTCTGCA	1565
Qy	1421	AGGCAGGCTGGCACGGGGTGGACTGCTCCATCAGATGTCCAGTGGCACATGGGGCTTTG	1480
Db	1566	AGGAAGGTTGGCAGCGTGGTAACTGCTCTGTGCCCTGCCACCCGGAACCTGGGGCTTCA	1625
Qy	1481	GCTGTAACCTTAACATGCCAGTGCCTCAACGGGGGAGCCTGCAACACCTGGACGGGACCT	1540
Db	1626	GTTGCAATGCCAGCTGCCAGTGTGCCCATGAGGCAGTCTGCAGCCCCAACTGGAGCCT	1685
Qy	1541	GCACGTGTGCACCTGGATGGCGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGT	1600


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; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 1976
; LENGTH: 1970
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1890)..(1890)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1970)..(1970)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-1976

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Query Match          15.8%; Score 540.6; DB 14; Length 1970;
Best Local Similarity 69.4%; Pred. No. 4.1e-164;
Matches 735; Conservative 0; Mismatches 324; Indels 0; Gaps 0;

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Qy      917 GGTGCCAGGATGAGTGTCTGTTGGGACCTATGGCGTTCTCTGTGCTGAGACCTGCCAGT 976
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Db      1498 GGTGCCAAGAGGAGTGCCCCTTCGGGTCCTTCGGCTTCCAGTGCTCACAGCGCTGTGACT 1439

Qy      977 GTGTCAACGGAGGGAAGTGTTACCACGTGAGCGGCGCATGCCCTCTGTGAAGCAGGCTTTG 1036
        | ||| || ||| ||||| | | | | || || || || || || || ||
Db      1438 GCCACAATGGGGGGCAGTGTTACCCACCACGGGTGCCTGCGAGTGTGAGCCTGGCTACA 1379

Qy      1037 CTGGCGAGCGCTGCGAAGCACGCCTGTGTCTGAGGGGCTCTACGGCATCAAATGTGACA 1096
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Db      1378 AGGGCCCACGCTGCCAGGAGCGACTGTGCCCGGAGGGCCTGCATGGCCCAGGCTGCACCC 1319

Qy      1097 AACGGTGTCCCTGCCACTTGGAACAACTCATAGCTGTCACCCCATGTCTGGAGAGTGTG 1156
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Db      1318 TGCCCTGCCCCTGTGACGCTGACAACACCATCAGCTGCCACCCAGTAAGTGGAGCTTGTA 1259

Qy      1157 CCTGCAAGCCGGGCTGGTCAGGACTCTACTGTAATGAGACATGTTCTCCTGGATTCTACG 1216
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Db      1258 CCTGCCAGCCAGGCTGGTCTGGTCACCACTGCAATGAATCCTGCCCTGTGGCTACTATG 1199

Qy      1217 GGGAAAGCTTGCCAGCAGATCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTGTGACTG 1276
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Db      1198 GCGATGGCTGCCAGCTGCCTTGACCTGTGAGAATGGCGCCGACTGCCACAGCATCACTG 1139

Qy      1277 GAAAGTGCACCTGTGCCCCAGGATTCAAAGGAATTGACTGCTCTACCCCATGCCCTCTGG 1336
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Db      1138 GGGGCTGCACTTGTGCTCCGGGCTTCATGGGAGAGGTCTGTGCCGTTTCCTGTGCAGCAG 1079

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; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 113
; LENGTH: 5036
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

; LOCATION: (230)...(3379)
US-09-796-753-113

Query Match 15.4%; Score 528.6; DB 10; Length 5036;
Best Local Similarity 58.3%; Pred. No. 6.1e-160;
Matches 987; Conservative 0; Mismatches 694; Indels 12; Gaps 3;

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Qy      515 GCTTCCGGGGCTGGCGCTGCGAGGACCGCTGTGAGCAGGGCACCTATGGTAACGACTGTC 574
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Db      771 GTTCCAGTGCCCCGAAGTGCCTTCAGCCCTGTACCCCTGGCTACTATGGCCCTGCCTGCC 830

Qy      575 ATCAGAGATGCCAGTGCCAGAATGGAGCCACCTGCGACCACGTACGGGGGAATGCCGCT 634
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Db      831 AGTTCGCTGCCAGTGCC---ATGGGGCACCTGCGATCCCCAGACTGGAGCCTGCTTCT 887

Qy      635 GCCCACCAGGATACACCGGAGCCTTCTGTGAGGATCTTTGTCCTCCTGGTAAACATGGTC 694
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      888 GCCCCGAGAGAGAACTGGGCCAGCTGTGACGTGTCTGTTCCAGGGCACTTCTGGCT 947

Qy      695 CACAGTGTGAGCAGAGATGCCCTTGTCAAATGGAGGAGTGTGTCATCACGTCACTGGAG 754
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      948 TCTTCTGCCCCAGCACCCATCCTTGCCAAAATGGAGGTGTCTTCCAAACCCACAGGGCT 1007

Qy      755 AATGCTCTTGCCCTTCTGGCTGGATGGGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTC 814
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1008 CCTGCAGCTGCCCCCTGGCTGGATGGGCACCATCTGCTCCCTGCCCTGCCAGAGGGCT 1067

Qy      815 GCTTTGGAAAGAACTGTTCCCAAGAATGCCAGTGCCATAATGGAGGGACGTGTGATGCTG 874
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Db     1068 TTCACGGACCCAAGTCTCCAGGAATGTCGCTGCCACAACGGCGGCCTCTGTGACCGAT 1127

Qy      875 CCACAGGCCAATGTCATTGCAGTCCAGGATACACAGGGGAACGGTGCCAGGATGAGTGTC 934
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Db     1128 TCACTGGGCAGTGCCGCTGCGCTCCGGGTTACACTGGGGATCGGTGCCGGGAGGAGTGCC 1187

Qy      935 CTGTTGGGACCTATGGCGTTCTCTGTGCTGAGACCTGCCAGTGTGTCAACGGAGGGAAGT 994
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Db     1188 CGGTGGGCCGCTTTGGGCGAGGACTGTGCTGAGACGTGCGACTGCGCCCCGGACGCCCGTT 1247

Qy      995 GTTACCACGTGAGCGGCGCATGCCTCTGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGAAG 1054
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Db     1248 GCTTCCCGGCCAACGGGCGCATGTCTGTGCAACACGGCTTCACTGGGGACCGCTGCACGG 1307

Qy     1055 CACGCCTGTGTCTGAGGGGCTCTACGGCATCAAATGTGACAAACGGTGTCCCTGCCACT 1114
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Db     1308 ATCGCTCTGCCCCGACGGCTTCTACGGTCTCAGCTGCCAGGCCCCCTGCACCTGCGACC 1367

Qy     1115 TGGAAAACACTCATAGCTGTCAACCCATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGT 1174
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Db     1368 GGGAGCACAGCCTCAGCTGCCACCCGATGAACGGGGAGTGCTCCTGCCTGCCGGGCTGGG 1427

Qy     1175 CAGGACTCTACTGTAATGAGACATGTTCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGA 1234
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Db     1428 CGGGCCTCCACTGCAACGAGAGCTGCCCCGAGGACACGCATGGGCCAGGGTGCCAGGAGC 1487

Qy     1235 TCTGCAGCTGCCAAAATGGGGCAGACTGTGACAGTGTGACTGGAAAGTGACCTGTGCCC 1294
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Db 1488 ACTGTCTCTGCCTGCACGGTGGCGTCTGCCAGGCTACCAGCGGCCTCTGTCACTGCGCGC 1547

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Db 1548 CGGGTTACACGGGCCCTCACTGTGCTAGTCTTTGTCTCCTGACACCTACGGTGTCAACT 1607

Qy 1355 GTTCCTCTCGCTGTGGCTGTAAAAATGATGCAGTCTGCTCTCCTGTGGACGGGTCTTGTA 1414
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Db 1608 GTTCTGCACGCTGCTCATGTGAAAATGCCATCGCCTGCTCACCCATCGACGGCGAGTGCG 1667

Qy 1415 CTTGCAAGGCAGGCTGGCACGGGGTGGACTGCTCCATCAGATGTCCCAGTGGCACATGGG 1474
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Db 1668 TCTGCAAGGAAGGTTGGCAGCGTGGTAACGTCTGTGCCCTGCCACCCGGAACCTGGG 1727

Qy 1475 GCTTTGGCTGTAACTTAACATGCCAGTGCCTCAACGGGGGAGCCTGCAACACCCTGGACG 1534
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Db 1728 GCTTCAGTTGCAATGCCAGCTGCCAGTGTGCCCATGAGGCAGTCTGCAGCCCCCAAAGT 1787

Qy 1535 GGACCTGCACGTGTGCACCTGGATGGCGCGGGGAGAAATGCGAACTTCCCTGCCAGGATG 1594
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Db 1788 GAGCCTGTACCTGCACCCCTGGGTGGCATGGGGCCCACTGCCAGCTGCCCTGTCCGAAGG 1847

Qy 1595 GCACGTACGGGCTGAACTGTGCTGAGCGCTGCGACTGCAGCCACGCAGATGGCTGCCACC 1654
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Db 1848 GGCAGTTTGGAGAAGGTTGTGCCAGTCGCTGTGACTGTGACCACTCTGATGGCTGTGACC 1907

Qy 1655 CTACCACGGGCCATTGCCGCTGCCTCCCGGGATGGTCAGGTGTCCACTGTGACAGCGTGT 1714
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Db 1908 CTGTTTCATGGACGCTGTCACTGCCAGGCTGGCTGGATGGGTGCCCGCTGCCACCTGTCT 1967

Qy 1715 GTGCTGAGGGACGCTGGGGCCCCAACTGCTCCCTGCCCTGCTACTGTAAAAATGGGGCTT 1774
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Db 1968 GCCCTGAGGGCTTATGGGGAGTCAACTGTAGCAACACCTGCACCTGCAAGAATGGGGGCA 2027

Qy 1775 CATGCTCCCCTGATGATGGCATCTGCGAGTGTGCACCAGGCTTCCGAGGCACCACTTGTC 1834
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Db 2028 CCTGTCTCCCTGAGAATGGCAACTGCGTGTGTGCACCCGGATTCCGGGGCCCCCTCCTGCC 2087

Qy 1835 AGAGGATCTGCTCCCCTGGTTTTTATGGGCATCGCTGCAGCCAGACATGCCCACAGTGCG 1894
| | | | | | | | | | | | | | | | | | | | | |

Db 2088 AGAGATCCTGTCAAGCCTGGCCGCTATGGCAAACGCTGTGTGCC-----CTGCAAGTGCG 2141

Qy 1895 TTCACAGCAGCGGGCCCTGCCACCACATCACCGGCCTGTGTGACTGCTTGCCTGGCTTCA 1954
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Db 2142 CTAACCACTCCTT---CTGCCACCCCTCGAACGGGACCTGCTACTGCCTGGCTGGCTGGA 2198

Qy 1955 CAGGCGCCCTCTGCAATGAAGTGTGTCCAGTGGCAGATTTGGGAAAAACTGTGCAGGAA 2014
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Db 2199 CAGGCCCCGACTGCTCCCAGCCATGCCCTCCAGGACACTGGGGAGAAAACTGTGCCCAGA 2258

Qy 2015 TTTGTACCTGCACCAACAACGGAACCTGTAACCCATTGACAGATCTTGTCACTGTTACC 2074
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Db 2259 CCTGCCAATGTCAACATGGTGGGACCTGCCATCCCAGGATGGGAGCTGTATCTGCCCCC 2318

Qy 2075 CCGGTTGGATTGGCAGTGACTGCTCTCAACCATGTCCACCTGCCCCTGGGGCCCCAACT 2134
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Db 2319 TAGGCTGGACTGGACACCACTGCTTAGAAGGCTGCCCTCTGGGGACATTTGGTGCTAACT 2378


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Qy      2135 GCATCCACACGTGCAACTGCCATAATGGAGCTTTCTGCAGCGCCTACGATGGGGAATGTA 2194
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Db      2379 GCTCCCAGCCATGCCAGTGTGGTCCTGGAGAAAAGTGCCACCCAGAGACTGGGGCCTGTG 2438

Qy      2195 AATGCACTCCTGG 2207
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Db      2439 TATGTCCCCCAGG 2451

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RESULT 14

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US-09-833-381-1910/c
; Sequence 1910, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1910
; LENGTH: 5197
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(5197)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1910

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Query Match          15.3%; Score 524.6; DB 9; Length 5197;
Best Local Similarity 58.0%; Pred. No. 1.3e-158;
Matches 972; Conservative 0; Mismatches 694; Indels 11; Gaps 2;

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Qy      591 CCAGAATGGAGCCACCTGCGACCACGTACGGGGGAATGCCGCTGCCACCAGGATACAC 650
          || |||| || ||||| | | || | | || ||||| || |
Db      4183 CC---ATGGGGCACCCCTGCGATCCCAGACTGGAGCCTGCTTCTGCCCCGAGAGAGAAC 4127

Qy      651 CGGAGCCTTCTGTGAGGATCTTTGTCCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAG 710
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Db      4126 TGGGCCCAGCTGTGACGTGTCCTGTTCCCAGGGCACTTCTGGCTTCTTCTGCCCCAGCAC 4067

Qy      711 ATGCCCTTGTCAAAATGGAGGAGTGTGTATCACGTCACTGGAGAATGCTCTTGCCCTTC 770
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Qy      771 TGGCTGGATGGGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTGGAAAGAACTG 830
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Db      4006 TGGCTGGATGGGCACCATCTGCTCCCTGCCCTGCCAGAGGGCTTTCACGGACCCAACTG 3947

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Qy 831 TTCCAAGAATGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAGGCCAATGTCA 890
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 Db 3946 CTCCCAGGAATGTCGCTGCCACAACGGCGGCCTCTGTGACCGATTCACTGGGCAGTGCCG 3887

Qy 891 TTGCAGTCCAGGATACACAGGGGAACGGTGCCAGGATGAGTGTCTTGGGACCTATGG 950
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 Db 3886 CTGCGCTCCGGGTACACTGGGGATCGGTGCCGGGAGGAGTGCCCGGTGGGCCGCTTTGG 3827

Qy 951 CGTTCTCTGTGCTGAGACCTGCCAGTGTGTCAACGGAGGGAAGTGTACCACGTGAGCGG 1010
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 Db 3826 GCAGGACTGTGCTGAGACGTGCGACTGCGCCCCGACGCCCGTGTCTTCCCGGCCAACGG 3767

Qy 1011 CGCATGCCTCTGTGAAGCAGGCTTTGCTGGCGAGCGCTGCGAAGCACGCCTGTGTCTCTGA 1070
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 Db 3766 CGCATGTCTGTGCGAACACGGCTTCACTGGGGACCGCTGCACGGATCGCCTCTGCCCCGA 3707

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 Db 3646 CTGCCACCCGATGAACGGGGAGTGCTCCTGCCTGCCGGGTGGGCGGGCCTCCACTGCAA 3587

Qy 1191 TGAGACATGTTCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCAGCTGCCAAAA 1250
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 Db 3586 CGAGAGCTGCCCCGAGGACACGCATGGGCCAGGTGCCAGGAGCACTGTCTCTGCCTGCA 3527

Qy 1251 TGGGGCAGACTGTGACAGTGTGACTGGAAAGTGCACCTGTGCCCCAGGATTCAAAGGAAT 1310
 || | || || | | | || || || || || || || || || ||
 Db 3526 CGGTGGCGTCTGCCAGGCTACCAGCGGCCTCTGTCACTGCGCGCCGGGTACACGGGGCC 3467

Qy 1311 TGA CTGCTCTACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCTCTCGCTGTGG 1370
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 Db 3466 TCACTGTGCTAGTCTTTGTCTCTGACACCTACGGTGTCAACTGTTCTGCACGCTGCTC 3407

Qy 1371 CTGTAAAAATGATGCAGTCTGCTCTCCTGTGGACGGGTCTTGTACTTGCAAGGCAGGCTG 1430
 ||| ||||| | ||||| || | |||| || ||||| || || ||
 Db 3406 ATGTGAAAATGCCATCGCCTGCTCACCCATCGACGGCGAGTGCGTCTGCAAGGAAGGTTG 3347

Qy 1431 GCACGGGGTGGACTGCTCCATCAGATGTCCAGTGGCACATGGGGCTTTGGCTGTAACTT 1490
 ||| | | ||||| | || || || || || ||||| || || ||
 Db 3346 GCAGCGTGGTAACCTGCTCTGTGCCCTGCCACCCGGAACCTGGGGCTTCAGTTGCAATGC 3287

Qy 1491 AACATGCCAGTGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCTGCACGTGTGC 1550
 | ||||| || | | || || ||||| || || || || || || ||
 Db 3286 CAGCTGCCAGTGTGCCCATGAGGCAGTCTGCAGCCCCCAAACCTGGAGCCTGTACCTGCAC 3227

Qy 1551 ACCTGGATGGCGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGTACGGGCTGAA 1610
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 Db 3226 CCCTGGGTGGCATGGGGCCCACTGCCAGCTGCCCTGTCCGAAGGGGAGTTTGGAGAAGG 3167

Qy 1611 CTGTGCTGAGCGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCACGGGCCATTG 1670
 ||||| |||| |||| |||| | ||||| |||| || || || ||
 Db 3166 TTGTGCCAGTCGCTGTGACTGTGACCACTCTGATGGCTGTGACCCTGTTTCATGGACGCTG 3107

Qy 1671 CCGCTGCCTCCCGGGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTGAGGGACGCTG 1730
 | | | | | | | | | | | | | | | | | | | | | |
 Db 3106 TCAGTGCCAGGCTGGCTGGATGGGTGCCCCTGCCACCTGTCTGCCCTGAGGGCTTATG 3047

Qy 1731 GGGCCCCAACTGCTCCCTGCCCTGCTACTGTAAAAATGGGGCTTCATGCTCCCCTGATGA 1790
 | | | | | | | | | | | | | | | | | | | | | |
 Db 3046 GGGAGTCAACTGTAGCAACACCTGCACCTGCAAGAATGGGGGCACCTGTCTCCCTGAGAA 2987

Qy 1791 TGGCATCTGCGAGTGTGCACCAGGCTTCCGAGGCACCACTTGTGAGAGGATCTGCTCCCC 1850
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 Db 2986 TGGCAACTGCGTGTGTGCACCCGGATTCCGGGGCCCCCTCCTGCCAGAGATCCTGTGAGCC 2927

Qy 1851 TGGTTTTTATGGGCATCGCTGCAGCCAGACATGCCACAGTGCCTTACAGCAGCGGGCC 1910
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 Db 2926 TGGCCGCTATGGCAAACGCTGTG-----TGCCCTGCAAGTGCCTAACCCTCCTTC 2875

Qy 1911 CTGCCACCACATCACCGGCCTGTGTGACTGCTTGCCTGGCTTACAGGCGCCCTCTGCAA 1970
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2874 TGCCACCCCTTCGAACGGGACCTGCTACTGCCTGGCTGGCTGGACAGGCCCCGACTGCTC 2815

Qy 1971 TGAAGTGTGTCCAGTGGCAGATTTGGGAAAAACTGTGCAGGAATTTGTACCTGCACCAA 2030
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 Db 2814 CCAGCCATGCCCTCCAGGACACTGGGGAGAAAACTGTGCCCAGACCTGCCAATGTACCA 2755

Qy 2031 CAACGGAACCTGTAACCCCATTGACAGATCTTGTCAGTGTTACCCCGGTTGGATTGGCAG 2090
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 Db 2754 TGGTGGGACCTGCCATCCCAGGATGGGAGCTGTATCTGCCCCCTAGGCTGGACTGGACA 2695

Qy 2091 TGAAGTGTGTCCAGTGGCAGATTTGGGAAAAACTGTGCAGGAATTTGTACCTGCACCAA 2150
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 Db 2694 CCACTGCTTAGAAGGCTGCCCTCTGGGGACATTTGGTGCTAACTGCTCCCAGCCATGCCA 2635

Qy 2151 CTGCCATAATGGAGCTTTCTGCAGCGCCTACGATGGGGAATGTAAATGCACTCCTGG 2207
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 Db 2634 GTGTGGTCCTGGAGAAAAGTGCCACCCAGAGACTGGGGCCTGTGTATGTCCCCCAGG 2578

RESULT 15

US-10-052-648A-1

; Sequence 1, Application US/10052648A

; Publication No. US20040005558A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, David
 ; APPLICANT: Burgess, Catherine
 ; APPLICANT: Casman, Stacie
 ; APPLICANT: Colman, Steven
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: Ellerman, Karen
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 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: MacDougall, John R.
 ; APPLICANT: Mehraban, Fuad
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Rothenberg, Mark
 ; APPLICANT: Shimkets, Richard
 ; APPLICANT: Smithson, Glennda

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; APPLICANT:  Spytek, Kimberly A.
; APPLICANT:  Stone, David J.
; APPLICANT:  Vernet, Corine A.M.
; APPLICANT:  Zerhusen, Bryan D.
; TITLE OF INVENTION:  PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
; TITLE OF INVENTION:  USING THE SAME
; FILE REFERENCE:  21402-250 (CURA-550)
; CURRENT APPLICATION NUMBER:  US/10/052,648A
; CURRENT FILING DATE:  2002-12-09
; PRIOR APPLICATION NUMBER:  60/262,454
; PRIOR FILING DATE:  2001-01-18
; PRIOR APPLICATION NUMBER:  60/272,920
; PRIOR FILING DATE:  2001-03-02
; PRIOR APPLICATION NUMBER:  60/284,549
; PRIOR FILING DATE:  2001-04-18
; PRIOR APPLICATION NUMBER:  60/303,229
; PRIOR FILING DATE:  2001-07-05
; PRIOR APPLICATION NUMBER:  60/262,892
; PRIOR FILING DATE:  2001-01-19
; PRIOR APPLICATION NUMBER:  60/263,605
; PRIOR FILING DATE:  2001-01-23
; PRIOR APPLICATION NUMBER:  60/269,098
; PRIOR FILING DATE:  2001-02-15
; PRIOR APPLICATION NUMBER:  60/264,159
; PRIOR FILING DATE:  2001-01-25
; PRIOR APPLICATION NUMBER:  60/265,517
; PRIOR FILING DATE:  2001-01-31
; PRIOR APPLICATION NUMBER:  60/271,855
; PRIOR FILING DATE:  2001-02-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS:  97
; SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH:  3063
;   TYPE:  DNA
;   ORGANISM:  Homo sapiens
US-10-052-648A-1
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Query Match          14.9%;  Score 511;  DB 15;  Length 3063;
Best Local Similarity  55.2%;  Pred. No. 2.4e-154;
Matches 1164;  Conservative    0;  Mismatches  850;  Indels    93;  Gaps    5;
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Qy      62 GGACAGCATCACCTCTGAATCTTGAAGACCCTAATGTGTGTAGCCACTGGGAAAGCTACT 121
      ||  ||  | |||| || |  || || ||  || |||  ||||| ||||| |
Db      47 GGCTGGCTGGAACCTCTCAACCCAGTGATCCCAATACCTGCAGCTTCTGGGAAAGCTTCA 106

Qy     122 CAGTGACTGTGCAAGAGTCATACCCACATCCCTTTGATCAAATTTACTACACGAGCTGC- 180
      |  ||  | |||| || | | ||||  |  |  ||  | ||||
Db     107 CTACCACCACCAAGGAGTCCCACTCCCGCCCTTCAGCCTGCTCCCTCAGAGCCCTGCG 166

Qy     181 --ACTGACATTCTAAACTGGTTTAAATGCACGCGGCACAGAGTCAGCTATCGGACAGCCT 238
      |  |  |  || ||| | | || | ||  || ||||| | |
Db     167 AGCGGCCCTGGGAGGGCCCCCATACTTGCCCCAGCCACGGTTGTATACGGACCGTGT 226

Qy     239 ATCGACATGGGGAGAAGACTATGTATAGGCGCAAGTCTCAGTGTTCCTGGATTTTATG 298
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Db     227 ACCGTCAGGTGGTGAAGACGGACCACCGCCAGCGCCTGCAGTGCTGCCATGGCTTCTATG 286
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Qy	299	AAAGCGGGGAAATGTGTGTCCCCCACTGTGCTGATAAAATGTGTCCATGGTCGCTGTATTG	358
Db	287	AGAGCAGGGGTTCTGTGTCCCGCTCTGTGCCAGGAGTGTGTCCATGGCCGTTGTGTGG	346
Qy	359	CTCCAAACACCTGTCACTGTGAGCCTGGCTGGGGAGGGACCAACTGCTCCAGTGCCTGCG	418
Db	347	CACCCAATCAGTGCCAATGTGTGCCAGGCTGGCGGGGCGACGACTGTTCCAGTGAGTGTG	406
Qy	419	ATGGTGATCACTGGGGTCCCCACTGCACCAGCCGGTGCCAGTGCAAAAATGGGGCTCTGT	478
Db	407	CCCCAGGAATGTGGGGGCCACAGTGTGACAAGCCCTGCAGCTGCGGCAACAACAGCTCGT	466
Qy	479	GCAACCCCATCACCGGGGCTTGCCACTGTGCTGCGGGCTTCCGGGGCTGGCGCTGCGAGG	538
Db	467	GTGATCCCAAGAGTGGGGTATGTTCTTGCCCTTCTGGTCTGCAGCCCCGAACTGCCTTC	526
Qy	539	ACCGCTGTGAGCAGGGGCACCTATGGTAACGACTGTCATCAGAGATGCCAGTGCCAGAATG	598
Db	527	AGCCCTGTACCCCTGGCTACTATGGCCCTGCCTGCCAGTTCGGCTGCCAGTGCC---ATG	583
Qy	599	GAGCCACCTGCGACCACGTACGGGGGAATGCCGCTGCCCACCAGGATACACCGGAGCCT	658
Db	584	GGGCACCTGCGATCCCCAGACTGGAGCCTGCTTCTGCCCCGAGAGAGAACTGGGCCCCA	643
Qy	659	TCTGTGAGGATCTTTGTCTCTCCTGGTAAACATGGTCCACAGTGTGAGCAGAGATGCCCTT	718
Db	644	GCTGTGACGTGTCTCTGTTCCAGGGCACTTCTGGCTTCTTCTGCCCCAGCACCCATTCTT	703
Qy	719	GTCAAAATGGAGGAGTGTGTTCATCACGTCACTGGAGAATGCTCTTGCCCTTCTGGCTGGA	778
Db	704	GCCAAATGGAGGTGTCTTCCAAACCCACAGGGCTCCTGCAGCTGCCCCCTGGCTGGA	763
Qy	779	T-----	779
Db	764	TGGTATGGAGGTTGGGGCCTGTGGGCATGGGGTGTGGGTCTGGGGAGAATTCTGTGGGTG	823
Qy	780	-----GGGCACAGTGTGTGGTCAGCCTTGCCCCGAGGGTCGCTTTG	820
Db	824	GTGCTAAGCAGGGCTCCAAGGGCACCATCTGCTCCCTGCCCTGCCAGAGGGCTTTCACG	883
Qy	821	GAAAGAACTGTTCCCAAGAATGCCAGTGCCATAATGGAGGGACGTGTGATGCTGCCACAG	880
Db	884	GACCCAATGCTCCCAGGAATGTCGCTGCCACAACGGCGGCCTCTGTGACCGATTCACTG	943
Qy	881	GCCAATGTCATTGCAGTCCAGGATACACAGGGGAACGGTGCCAGGATGAGTGTCTCTGTTG	940
Db	944	GGCAGTGCCGCTGCGCTCCGGGTTAACTGGGGATCGGTGCCGGGAGGAGTGCCCGGTGG	1003
Qy	941	GGACCTATGGCGTTCTCTGTGCTGAGACCTGCCAGTGTGTCAACGGAGGGAAGTGTTACC	1000
Db	1004	GCCGCTTTGGGCAGGACTGTGCTGAGACGTGCGACTGCGCCCCGGACGCCCGTTGCTTCC	1063
Qy	1001	ACGTGAGCGGGCGCATGCCTCTGTGAAGCAGGCTTTGCTGGCGAGCGCTGCCAAGCACGCC	1060
Db	1064	CGGCCAACGGCGCATGTCTGTGCGAACACGGCTTCACTGGGGACCGCTGCACGGATCGCC	1123

Qy	1061	TGTGTCCTGAGGGGCTCTACGGCATCAAATGTGACAAACGGTGTCCCTGCCACTTGGAAA	1120
Db	1124	TCTGCCCCGACGGCTTCTACGGTCTCAGCTGCCAGGCCCTGCACCTGCGACCGGGAGC	1183
Qy	1121	ACACTCATAGCTGTCACCCCATGTCTGGAGAGTGTGCCTGCAAGCCGGGCTGGTCAGGAC	1180
Db	1184	ACAGCCTCAGCTGCCACCCGATGAACGGGAGTGCTCCTGCCTGCCGGGCTGGGCGGGCC	1243
Qy	1181	TCTACTGTAATGAGACATGTTCTCCTGGATTCTACGGGGAAGCTTGCCAGCAGATCTGCA	1240
Db	1244	TCCACTGCAACGAGAGCTGCCCGCAGGACACGCATGGGCCAGGGTGCCAGGAGCACTGTC	1303
Qy	1241	GCTGCCAAAATGGGGCAGACTGTGACAGTGTGACTGGAAAGTGCACCTGTGCCCCAGGAT	1300
Db	1304	TCTGCCTGCACGGTGGCGTCTGCCAGGCTACCAGCGGCCCTCTGTCACTGCGCGCCGGGTT	1363
Qy	1301	TCAAAGGAATTGACTGCTCTACCCCATGCCCTCTGGGAACCTATGGGATAAACTGTTCCCT	1360
Db	1364	ACACGGGCCCTCACTGTGCTAGTCTTTGTCTCTGACACCTACGGTGTCAACTGTTCTG	1423
Qy	1361	CTCGCTGTGGCTGTAAAAATGATGCAGTCTGCTCTCCTGTGGACGGGTCTTGTACTTGCA	1420
Db	1424	CACGCTGCTCATGTGAAAATGCCATCGCCTGCTCACCCATCGACGGCGAGTGCCTCTGCA	1483
Qy	1421	AGGCAGGCTGGCACGGGGTGGACTGCTCCATCAGATGTCCCAGTGGCACATGGGGCTTTG	1480
Db	1484	AGGAAGGTTGGCAGCGTGGTAACTGCTCTGTGCCCTGCCCCACCCGGAACCTGGGGCTTCA	1543
Qy	1481	GCTGTAACTTAACATGCCAGTGCCTCAACGGGGGAGCCTGCAACACCCTGGACGGGACCT	1540
Db	1544	GTTGCAATGCCAGCTGCCAGTGTGCCCATGAGGCAGTCTGCAGCCCCCAAACCTGGAGCCT	1603
Qy	1541	GCACGTGTGCACCTGGATGGCGCGGGGAGAAATGCGAACTTCCCTGCCAGGATGGCACGT	1600
Db	1604	GTACCTGCACCCCTGGGTGGCATGGGGCCCACTGCCAGCTGCCCTGTCCGAAGGGGCAGT	1663
Qy	1601	ACGGGCTGAACTGTGCTGAGCGCTGCGACTGCAGCCACGCAGATGGCTGCCACCCTACCA	1660
Db	1664	TTGGAGAAGGTTGTGCCAGTCGCTGTGACTGTGACCACTCTGATGGCTGTGACCCTGTTC	1723
Qy	1661	CGGGCCATTGCCGCTGCCTCCCGGGATGGTCAGGTGTCCACTGTGACAGCGTGTGTGCTG	1720
Db	1724	ATGGACGCTGTCACTGCCAGGCTGGCTGGATGGGTGCCCGCTGCCACCTGTCTGCCCTG	1783
Qy	1721	AGGGACGCTGGGGCCCCAACTGCTCCCTGCCCTGCTACTGTAAAAATGGGGCTTCATGCT	1780
Db	1784	AGGGCTTATGGGGAGTCAACTGTAGCAACACCTGCACCTGCAAGAATGGGGGCACCTGTC	1843
Qy	1781	CCCCTGATGATGGCATCTGCGAGTGTGCACCAGGCTTCCGAGGCACCACTTGTGAGAGGA	1840
Db	1844	TCCCTGAGAATGGCAACTGCGTGTGTGCACCCGGATTCCGGGGCCCCCTCCTGCCAGAGAT	1903
Qy	1841	TCTGCTCCCCTGGTTTTTATGGGCATCGCTGCAGCCAGACATGCCACAGTGCCTTACCA	1900
Db	1904	CCTGTCAGCCTGGCCGCTATGGCAAACGCTGTGTGC-----CCTGCAAGTGCCTAACC	1957
Qy	1901	GCAGCGGGCCCTGCCACCACATCACCGGCCCTGTGTGACTGCTTGCTGGCTTCACAGGCG	1960

Db	1958	ACTCC---TTCTGCCACCCCTCGAACGGGACCTGCTACTGCCTGGCTGGCTGGACAGGCC	2014
Qy	1961	CCCTCTGCAATGAAGTGTGTCCCAGTGGCAGATTTGGGAAAACTGTGCAGGAATTTGTA	2020
Db	2015	CCGACTGCTCCCAGCGCTGCCCTCTGGGGACATTTGGTGCTAACTGCTCCCAGCCATGCC	2074
Qy	2021	CCTGCACCAACAACGGAACCTGTAACCCCATTTGACAGATCTTGTCAGTGTTACCCCGGTT	2080
Db	2075	AGTGTGGTCCTGGAGAAAAGTGCCACCCAGAGACTGGGGCCTGTGTATGTCCCCCAGGGC	2134
Qy	2081	GGATTGG	2087
Db	2135	ACAGTGG	2141

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Job time : 1167 secs